



## SEQUENCE LISTING

<110> Bejanin, Stephane  
Tanaka, Hiroaki

<120> CYTOGRAM POLYPEPTIDES AND USES THEREOF

<130> G-142US05REG

<140> US 09/978,418

<141> 2001-10-15

<150> US 60/311,305

<151> 2001-08-10

<150> US 60/314,734

<151> 2001-08-24

<150> US 60/318,204

<151> 2001-09-07

<150> US 60/326,470

<151> 2001-10-01

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gta att tcc tgt gca aaa gac gga gtg aaa ttt tct gca agt gga gaa 332
Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu
25          30          35
ctt gga aat gga aac att aaa ttg tca cag aca agt aat gtc gat aaa 380
Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys
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55          60          65
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Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser
70          75          80
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Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu
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Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys
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Ile Glu Asp Glu Glu Gly Ser
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&lt;212&gt; PRT

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35          40          45
Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro
50          55          60
Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala
65          70          75          80
Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro
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                               Met Gln Asp Glu Asp Gly Tyr Ile
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acc tta aat att aaa act cgg aaa cca gct ctc gtc tcc gtt ggc tct 162
Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val Ser Val Gly Ser
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Ala Ser Ser Ser Trp Trp Arg Val Met Ala Leu Ile Leu Leu Ile Leu
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Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val
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ctg caa caa tta gca aag cgc ttc tgt caa tat gtg gta aaa caa tca 354
Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser
75           80           85

gaa cta aag ggc act ttc aaa ggt cat aaa tgc agc ccc tgt gac aca 402
Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr
90           95           100

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Asn Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
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act cat tta att cgt tgg gtc gga tta tct cgc cag aag tcg aat gag 594
Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu
      155      160      165
gtc tgg aag tgg gag gat ggc tcg gtt atc tca gaa aat atg ttt gag 642
Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu
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ttt ttg gaa gat gga aaa gga aat atg aat tgt gct tat ttt cat aat 690
Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn
      185      190      195      200
ggg aaa atg cac cct acc ttc tgt gag aac aaa cat tat tta atg tgt 738
Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys
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gag agg aag gct ggc atg acc aag gtg gac caa cta cct taatgcaaag 787
Glu Arg Lys Ala Gly Met Thr Lys Val Asp Gln Leu Pro
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      35      40      45
Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp
      50      55      60
Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
      65      70      75      80
Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly
      85      90      95
His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
      100      105      110
Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
      115      120      125
Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn
      130      135      140
Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly
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Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn
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taaaaatgga acactgaaag acacagagtt tttattttca gcactgcagc tctg atg 237  
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1  
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Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro  
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Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro His  
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Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser Phe  
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ata atg gca gtg ggt gag ccc ctg gtg cac atc agg gtc act ctt ctg 429  
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Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser Tyr  
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Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val Asn  
115 120 125  
aag ctg ttg ttt gct gca cac ctt cct gtg ttc acc tac aca gag cag 669  
Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu Gln  
130 135 140 145

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Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val Tyr	
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Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val Tyr	
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Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly Leu	
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245 250 255	
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390 395 400	
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Tyr	Pro	Gly	Asn	Ile	Phe	Arg	Leu	Lys	Tyr	Cys	Gly	Asn	Leu	Val	Val		
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Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu Val
          740          745          750
gct ttt tta tta ttt tgc tta cat gtg ctt ttt aag aaa cgc aca aaa 2541
Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr Lys
          755          760          765
agt aaa gaa gat gaa gaa gga taagagaaat gggaaaaaga aggagactaa 2592
Ser Lys Glu Asp Glu Glu Gly
770          775
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Phe Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu
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Leu Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln
65          70          75          80
Ala Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu
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Lys Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser
          100          105          110
Tyr Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val
          115          120          125
Asn Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu
          130          135          140
Gln His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr
145          150          155          160
Tyr His Gly Tyr Val Glu Gly Val Pro Glu Ser Leu Val Ala Leu Ser
          165          170          175
Thr Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val
          180          185          190
Tyr Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val
          195          200          205
Tyr Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly

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210	215	220
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Arg Phe Val Glu Leu Val Val Val Val	Asp Asn Ile Arg Tyr Leu Phe	
260	265	270
Ser Gln Ser Asn Ala Thr Thr Val Gln His Glu Val Phe Asn Val Val		
275	280	285
Asn Ile Val Asp Ser Phe Tyr His Pro Leu Glu Val Asp Val Ile Leu		
290	295	300
Thr Gly Ile Asp Ile Trp Thr Ala Ser Asn Pro Leu Pro Thr Ser Gly		
305	310	315
Asp Leu Asp Asn Val Leu Glu Asp Phe Ser Ile Trp Lys Asn Tyr Asn		
325	330	335
Leu Asn Asn Arg Leu Gln His Asp Val Ala His Leu Phe Ile Lys Asp		
340	345	350
Thr Gln Gly Met Lys Leu Gly Val Ala Tyr Val Lys Gly Ile Cys Gln		
355	360	365
Asn Pro Phe Asn Thr Gly Val Asp Val Phe Glu Asp Asn Arg Leu Val		
370	375	380
Val Phe Ala Ile Thr Leu Gly His Glu Leu Gly His Asn Leu Gly Met		
385	390	395
Gln His Asp Thr Gln Trp Cys Val Cys Glu Leu Gln Trp Cys Ile Met		
405	410	415
His Ala Tyr Arg Lys Val Thr Thr Lys Phe Ser Asn Cys Ser Tyr Ala		
420	425	430
Gln Tyr Trp Asp Ser Thr Ile Ser Ser Gly Leu Cys Ile Gln Pro Pro		
435	440	445
Pro Tyr Pro Gly Asn Ile Phe Arg Leu Lys Tyr Cys Gly Asn Leu Val		
450	455	460
Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Thr Ile Arg Gln Cys Ala		
465	470	475
Lys Asp Pro Cys Cys Leu Leu Asn Cys Thr Leu His Pro Gly Ala Ala		
485	490	495
Cys Ala Phe Gly Ile Cys Cys Lys Asp Cys Lys Phe Leu Pro Ser Gly		
500	505	510
Thr Leu Cys Arg Gln Gln Val Gly Glu Cys Asp Leu Pro Glu Trp Cys		
515	520	525
Asn Gly Thr Ser His Gln Cys Pro Asp Asp Val Tyr Val Gln Asp Gly		
530	535	540
Ile Ser Cys Asn Val Asn Ala Phe Cys Tyr Glu Lys Thr Cys Asn Asn		
545	550	555
His Asp Ile Gln Cys Lys Glu Ile Phe Gly Gln Asp Ala Arg Ser Ala		
565	570	575
Ser Gln Ser Cys Tyr Gln Glu Ile Asn Thr Gln Gly Asn Arg Phe Gly		
580	585	590
His Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp		
595	600	605
Ile Met Cys Gly Arg Val Gln Cys Glu Asn Val Gly Val Ile Pro Asn		
610	615	620
Leu Ile Glu His Ser Thr Val Gln Gln Phe His Leu Asn Asp Thr Thr		
625	630	635
Cys Trp Gly Thr Asp Tyr His Leu Gly Met Ala Ile Pro Asp Ile Gly		
645	650	655

Glu Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg  
                   660                  665                  670  
 Lys Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys  
                   675                  680                  685  
 Thr Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys  
                   690                  695                  700  
 Asn His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly  
 705                  710                  715                  720  
 Ser Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn  
                   725                  730                  735  
 Val Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu  
                   740                  745                  750  
 Val Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr  
                   755                  760                  765  
 Lys Ser Lys Glu Asp Glu Glu Gly  
                   770                  775

<210> 7  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..263

<220>  
 <221> CDS  
 <222> 264..926

<220>  
 <221> 3'UTR  
 <222> 927..1436

<220>  
 <221> polyA\_signal  
 <222> 1404..1409

<220>  
 <221> polyA\_site  
 <222> 1421..1436

<400> 7  
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 ccagccaggc tacagggatc gattggagct gtccttgggg ctgtaattgg cccagctga 120  
 gcagggcaaa cactgaggtc aactacaagc cacaggcccc ttccccagcc tcagttcaca 180  
 gctgccctgt tgcagggagg cgggtggcct tctgttgcta gaccgagcct gtgggatata 240  
 ccaaggcaga ggagcccata gcc atg agg agc ctc ggg gcc ctg ctc ttg ctg 293  
                                   Met Arg Ser Leu Gly Ala Leu Leu Leu Leu  
   -15                                  -10  
 ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca acg ccg ccc 341  
 Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro Thr Pro Pro  
                                   -5                                  1                                  5  
 gac aac atc caa gtg cag gaa aac ttc aat atc tct cgg atc tat ggg 389  
 Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly

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      10      15      20
aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg ctg aag aag 437
Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys
      25      30      35
atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485
Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly Glu Gly Ala
      40      45      50      55
aca gag gcg gag atc agc atg acc agc act cgt tgg cgg aaa ggt gtc 533
Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Lys Gly Val
      60      65      70
tgt gag gag acg tct gga gct tat gag aaa aca gat act gat ggg aag 581
Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys
      75      80      85
ttt ctc tat cac aaa tcc aaa tgg aac ata acc atg gag tcc tat gtg 629
Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Met Glu Ser Tyr Val
      90      95      100
gtc cac acc aac tat gat gag tat gcc att ttc ctg acc aag aaa ttc 677
Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe
      105      110      115
agc cgc cat cat gga ccc acc att act gcc aag ctc tac ggg cgg gcg 725
Ser Arg His His Gly Pro Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala
      120      125      130      135
ccg cag ctg agg gaa act ctc ctg cag gac ttc aga gtg gtt gcc cag 773
Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp Phe Arg Val Val Ala Gln
      140      145      150
ggt gtg ggc atc cct gag gac tcc atc ttc acc atg gct gac cga ggt 821
Gly Val Gly Ile Pro Glu Asp Ser Ile Phe Thr Met Ala Asp Arg Gly
      155      160      165
gaa tgt gtc cct ggg gag cag gaa cca gag ccc atc tta atc ccg aga 869
Glu Cys Val Pro Gly Glu Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg
      170      175      180
gtc cgg agg gct gct acc cca aga aga gga agg atc agg ggg tgg gca 917
Val Arg Arg Ala Ala Thr Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala
      185      190      195
act ggt aac tgaagtcacc aagaaagaag attcctgcca gctgggctac 966
Thr Gly Asn
200
tcggccggtc cctgcatggg aatgaccagc aggtattttct ataatggtac atccatggcc 1026
tgtgagactt tccagtacgg cggtgcatg ggcaacggta acaacttcgt cacagaaaag 1086
gagtgtctgc agacctgccg aactgtggcg gcctgcaatc tccccatagt ccggggcccc 1146
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gccggtctgc aagtcagagg atggccagtg tctgtcccg ggtcctgtgg caggcagcgc 1386
caagcaacct gggtccaaat aaaaactaaa ttgcaaaaaa aaaaaaaaaa 1436

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&lt;210&gt; 8

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..19

&lt;400&gt; 8

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Met Arg Ser Leu Gly Ala Leu Leu Leu Leu Leu Ser Ala Cys Leu Ala
              -15                      -10                      -5
Val Ser Ala Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln
              1                      5                      10
Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala
              15                      20                      25
Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr
30                      35                      40                      45
Val Ser Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser
              50                      55                      60
Met Thr Ser Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly
              65                      70                      75
Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser
              80                      85                      90
Lys Trp Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp
              95                      100                      105
Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro
110                      115                      120                      125
Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr
              130                      135                      140
Leu Leu Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu
              145                      150                      155
Asp Ser Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu
              160                      165                      170
Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Ala Thr
              175                      180                      185
Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala Thr Gly Asn
190                      195                      200

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&lt;210&gt; 9

&lt;211&gt; 2132

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 5'UTR

&lt;222&gt; 1..92

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 93..551

&lt;220&gt;

&lt;221&gt; 3'UTR

&lt;222&gt; 552..2132

&lt;220&gt;

&lt;221&gt; polyA\_signal

&lt;222&gt; 2085..2090

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 2117..2132

&lt;400&gt; 9

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gagatgtggt tctgcgcgtg tgcggacggc tgtctgttaa ctccgcggtc agttcccga . 60
ctggtggctg gtctgcaggg ttgacctgcg ca atg cag agg ctg cag gta gtg 113
                               Met Gln Arg Leu Gln Val Val
                               -35                               -30
ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg ccg cag gcc 161
Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met Pro Gln Ala
                               -25                               -20                               -15
gcg cct tgc ctg agc ggt gcc ccg cag gcc tgc gcc gcg gac gtg gtg 209
Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala Asp Val Val
                               -10                               -5                               1
gtg gtg cac ggg cgg cgc acg gcc atc tgc cgg gcg ggc cgc ggc ggc 257
Val Val His Gly Arg Arg Thr Ala Ile Cys Arg Ala Gly Arg Gly Gly
5                               10                               15                               20
ttc aag gac acc acc ccc gac gag ctt ctc tgc gca gtc atg acc gcg 305
Phe Lys Asp Thr Thr Pro Asp Glu Leu Leu Ser Ala Val Met Thr Ala
                               25                               30                               35
gtt ctc aag gac gtg aat ctg agg ccg gaa cag ctg ggg gac atc tgt 353
Val Leu Lys Asp Val Asn Leu Arg Pro Glu Gln Leu Gly Asp Ile Cys
                               40                               45                               50
gtc gga aat gtg ctg cag cct ggg gcc ggg gca atc atg gcc cga atc 401
Val Gly Asn Val Leu Gln Pro Gly Ala Gly Ala Ile Met Ala Arg Ile
                               55                               60                               65
gcc cag ttt ctg agt gac atc ccg gag act gtg cct ttg tcc act gtc 449
Ala Gln Phe Leu Ser Asp Ile Pro Glu Thr Val Pro Leu Ser Thr Val
                               70                               75                               80
aat aga cag tgt tgc tgc ggg cta cag gca gtg gcc agc ata gca ggg 497
Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Ser Ile Ala Gly
85                               90                               95                               100
tgg agt cca tgt ccc tgg ctg aca gag gga acc ctg gaa ata tta ctt 545
Trp Ser Pro Cys Pro Trp Leu Thr Glu Gly Thr Leu Glu Ile Leu Leu
                               105                               110                               115
cgc gct tgatggagaa ggagaaggcc agagattgcc tgattcctat ggggataacc 601
Arg Ala
tctgagaatg tggctgagcg gtttggcatt tcacgggaga agcaggatac ctttgccctg 661
gcttcccagc agaaggcagc aagagcccag agcaagggtc gtttccaagc tgagattgtg 721
cctgtgacca ccacggtcca tgatgacaag ggcaçcaaga ggagcatcac tgtgaccacg 781
gatgagggtg tccgccccag caccaccatg gagggcctgg ccaaactgaa gcctgccttc 841
aagaaagatg gttctaccac agctggttag actggtccgg ggtaggggta tgagaaagca 901
ggccatggcc atgctgggtg ctgtactctg ggaacctgga atagaccagg cccctctgca 961
aagtagaagt gggagggtg ggtatctctc atccccacc cgatgccttc ttacccaac 1021
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ctcacccttc tggaagagac acacaccagg cagcctgtag gcccatggat ggggtgggcc 1441
ccaggggagg cagagggcca gtgtgtcagc tcaggtcttt acctgtctg cagggtgac 1501
agttagtgac gtggacatct tgcagatcaa tgaggccttt gcaagccagg ctgcctactg 1561
tgtggagaag ctacgactcc cccctgagaa ggtgaacccc ctgggggggtg cagtggcctt 1621
agggcaccca ctgggctgca ctggggcacg acaggtcatc acgctgctca atgagctgaa 1681
gcgccgtggg aagagggcat acggagtggg gtccatgtgc atcgggactg gaatgggagc 1741
cgctgccgtc tttgaatacc ctgggaactg agtgaggtcc caggctggag gcgctacgca 1801
gacagtctct ctgctctagc agcaaggcag taacaccaca aaagcaaac cacatgggaa 1861

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aactcagcac tgggtggtggt ggcagtggac agatcaaggc acttcaactc atttggaata 1921
tgtgaacact gatgacatgg tataggagtg ggtgggggtgt tgagccaccc atcagaccct 1981
ctttagctgt gcaagataaa agcagcctgg gtcacccagg ccacaaggcc atggttaatt 2041
cttaaggcaa ggcaaattcca tggatgagaa gtgcaatggg catagtaaaa gtgcatgaat 2101
ttatcttaaa aaaagaaaaa aaaaaaaaaa a 2132

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<210> 10
<211> 153
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..35

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<400> 10
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
-35 -30 -25 -20
Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
-15 -10 -5
Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
1 5 10
Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
15 20 25
Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
30 35 40 45
Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
50 55 60
Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
65 70 75
Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln
80 85 90
Ala Val Ala Ser Ile Ala Gly Trp Ser Pro Cys Pro Trp Leu Thr Glu
95 100 105
Gly Thr Leu Glu Ile Leu Leu Arg Ala
110 115

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<210> 11
<211> 2266
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..200

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<220>
<221> CDS
<222> 201..986

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<220>
<221> 3'UTR
<222> 987..2266

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<220>

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&lt;221&gt; polyA\_signal

&lt;222&gt; 2233..2238

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 2251..2266

&lt;400&gt; 11

aacagagcta gactccgtct caagaagaag aagaaggaga agaaggagaa ggagaagggga 60  
 aaaaagaatc ctcatcatta atgcaagtgg aaggaaactc ttcaccaaag aattgatcac 120  
 atcatgaaag gtgaaatcat tacggaattg cttaaataata taatttgaat ctggatttaa 180  
 aaataataaa tgtgatcagg atg ccc ttc tct cat ctg tct acc tac agc ctg 233

Met Pro Phe Ser His Leu Ser Thr Tyr Ser Leu

-20

-15

gtt tgg gtc atg gca gca gtg gtg ctg tgc aca gca caa gtg caa gtg 281  
 Val Trp Val Met Ala Ala Val Val Leu Cys Thr Ala Gln Val Gln Val

-10

-5

1

gtg acc cag gat gaa aga gag cag ctg tac aca act gct tcc tta aaa 329  
 Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys  
 5 10 15 20

tgc tct ctg caa aat gcc cag gaa gcc ctc att gtg aca tgg cag aaa 377  
 Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys

25

30

35

aag aaa gct gta agc cca gaa aac atg gtc acc ttc agc gag aac cat 425  
 Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe Ser Glu Asn His

40

45

50

ggg gtg gtg atc cag cct gcc tat aag gac aag ata aac att acc cag 473  
 Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln

55

60

65

ctg gga ctc caa aac tca acc atc acc ttc tgg aat atc acc ctg gag 521  
 Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu

70

75

80

gat gaa ggg tgt tac atg tgt ctc ttc aat acc ttt ggt ttt ggg aag 569  
 Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys

atc tca gga acg gcc tgc ctc acc gtc tat gta cag ccc ata gta tcc 617  
 Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser

105

110

115

ctt cac tac aaa ttc tct gaa gac cac cta aat atc act tgc tct gcc 665  
 Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala

120

125

130

act gcc cgc cca gcc ccc atg gtc ttc tgg aag gtc cct cgg tca ggg 713  
 Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly

135

140

145

att gaa aat agt aca gtg act ctg tct cac cca aat ggg acc acg tct 761  
 Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser

150

155

160

gtt acc agc atc ctc cat atc aaa gac cct aag aat cag gtg ggg aag 809  
 Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys

gag gtg atc tgc cag gtg ctg cac ctg ggg act gtg acc gac ttt aag 857  
 Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp Phe Lys

185

190

195

caa acc gtc aac aaa ggc tat tgg ttt tca gtt ccg cta ttg cta agc 905  
 Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser

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      200      205      210
att gtt tcc ctg gta att ctt ctc gtc cta atc tca atc tta ctg tac      953
Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr
      215      220      225
tgg aaa cgt cac cgg aat cag gac cga gag ccc taaataagtc acacagcacc 1006
Trp Lys Arg His Arg Asn Gln Asp Arg Glu Pro
      230      235
ctgaaagtga ttccctgggc tacttgaatt tgacacaaga gaaaagcagg agaaaaaggg 1066
gccattctcc aaaggacctg aaagagcaaa agaggtggga gcgaaagcct taaggatccc 1126
acgacttttt actgccatct gagctactca gtgtttgaat cccaagagga agtcagttta 1186
cctctcaggt ctgttgtagg acttgatttt gtaaagcaat gccatgttat gtggttgaaa 1246
gggcactgga cttagttagt atcaggagca ctgagctcac agactgactt gggctcctac 1306
tggtggggac ctctgttagt cactttacct catccaaagt ataaaggaat tggaccaaatt 1366
aatttaccac atagctctaa aacttaattt aaaatgtaat tccagaaaaa aaaaggggaat 1426
aagcaaaggg ggaagaattg aaagagagag agaagaaaga atacagagag cttacctttt 1486
gcctttctgt tgatgttaca tctcttcttc ctatgttctt aggtctatga gtctgtttcc 1546
ccatcatttg gtatctagtc cagttcctgc ttactgcttt gctaatagct ggcccttgcta 1606
gaatccttgg ttctactgct gttcttcatg tgcttctatg agatttactc caacacaaat 1666
aggactgaat ttattgtgaa gtaacattgg caatcttaac ttattcattt aacttatttt 1726
tatagctaga taaatattgt tagtcttaga caatagctca cattttttga gaagcatgcc 1786
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cctcatataa tgaaaataca ttatgaaaac agatgtttag gagatttctt gtatagcagt 1906
cagccaattc atatgctttg tctctgctgg cttctttttc catgcgttaa cttttcccaa 1966
tagcagagga ggcaaatatg agcatacaat ccctttgttc taaagatatt gttccagcta 2026
gtggaatgat gttgaatctt taataacat aattagttgc tttttcagta tcttctgctt 2086
tgtctgtgtc tatccagtgg cctaggaatt aaagtgtgag ttgttttcgc tgttaaattg 2146
gatatttata tatatatata tagcaagatt ttcatgtgtt atttaattct gtattgtttc 2206
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<210> 12  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

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<400> 12
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      -20      -15      -10
Ala Val Val Leu Cys Thr Ala Gln Val Gln Val Val Thr Gln Asp Glu
      -5      1      5
Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys Cys Ser Leu Gln Asn
10      15      20      25
Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys Lys Lys Ala Val Ser
      30      35      40
Pro Glu Asn Met Val Thr Phe Ser Glu Asn His Gly Val Val Ile Gln
      45      50      55
Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn
      60      65      70
Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr
      75      80      85
Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys Ile Ser Gly Thr Ala
90      95      100      105

```



Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser Leu His Tyr Lys Phe  
                   110                  115                  120  
 Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala  
                   125                  130                  135  
 Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr  
                   140                  145                  150  
 Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser Val Thr Ser Ile Leu  
                   155                  160                  165  
 His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln  
 170                  175                  180                  185  
 Val Leu His Leu Gly Thr Val Thr Asp Phe Lys Gln Thr Val Asn Lys  
                   190                  195                  200  
 Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser Ile Val Ser Leu Val  
                   205                  210                  215  
 Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr Trp Lys Arg His Arg  
                   220                  225                  230  
 Asn Gln Asp Arg Glu Pro  
                   235

<210> 13  
 <211> 1597  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..65  
  
 <220>  
 <221> CDS  
 <222> 66..1334

<220>  
 <221> 3'UTR  
 <222> 1335..1597

<220>  
 <221> polyA\_signal  
 <222> 1558..1563

<220>  
 <221> polyA\_site  
 <222> 1582..1597

<400> 13  
 actactccag acagacggct ttggaatcca ccagctacat ccagctccct gaggcagagt 60  
 tgaga atg gag aga atg tta cct ctc ctg act ctg ggg ctc ttg gcg gct 110  
           Met Glu Arg Met Leu Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala  
                   -20                  -15                  -10  
 ggg ttc tgc cct gct gtc ctc tgc cac cct aac agc cca ctt gac gag 158  
 Gly Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu  
                   -5                  1                  5  
 gag aat ctg acc cag gag aac caa gac cga ggg aca cac gtg gac ctc 206  
 Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu  
           10                  15                  20

gga tta gcc tcc gcc aac gtg gac ttc gct ctc agc ctg tac aag cag	254
Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln	
25 30 35 40	
tta gtc ctg aag gcc cct gat aag aat gtc atc ttc tcc cca ctg agc	302
Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser	
45 50 55	
atc tcc acc gcc ttg gcc ttc ctg tct ctg ggg gcc cat aat acc acc	350
Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr	
60 65 70	
ctg aca gag att ctc aaa ggc ctc aag ttc aac ctc acg gag act tct	398
Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser	
75 80 85	
gag gca gaa att cac cag agc ttc cag cac ctc ctg cgc acc ctc aat	446
Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn	
90 95 100	
cag tcc agc gat gag ctg cag ctg agt atg gga aat gcc atg ttt gtc	494
Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val	
105 110 115 120	
aaa gag caa ctc agt ctg ctg gac agg ttc acg gag gat gcc aag agg	542
Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg	
125 130 135	
ctg tat ggc tcc gag gcc ttt gcc act gac ttt cag gac tca gct gca	590
Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala	
140 145 150	
gct aag aag ctc atc aac gac tac gtg aag aat gga act agg ggg aaa	638
Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys	
155 160 165	
atc aca gat ctg atc aag gac ctt gac tcg cag aca atg atg gtc ctg	686
Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu	
170 175 180	
gtg aat tac atc ttc ttt aaa gcc aaa tgg gag atg ccc ttt gac ccc	734
Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro	
185 190 195 200	
caa gat act cat cag tca agg ttc tac ttg agc aag aaa aag tgg gta	782
Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val	
205 210 215	
atg gtg ccc atg atg agt ttg cat cac ctg act ata cct tac ttc cgg	830
Met Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg	
220 225 230	
gac gag gag ctg tcc tgc acc gtg gtg gag ctg aag tac aca ggc aat	878
Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn	
235 240 245	
gcc agc gca ctc ttc atc ctc cct gat caa gac aag atg gag gaa gtg	926
Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val	
250 255 260	
gaa gcc atg ctg ctc cca gag acc ctg aag cgg tgg aga gac tct ctg	974
Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu	
265 270 275 280	
gag ttc aga gag ata ggt gag ctc tac ctg cca aag ttt tcc atc tcg	1022
Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser	
285 290 295	
agg gac tat aac ctg aac gac ata ctt ctc cag ctg ggc att gag gaa	1070
Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu	
300 305 310	
gcc ttc acc agc aag gct gac ctg tca ggg atc aca ggg gcc agg aac	1118

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Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn
      315                320                325
cta gca gtc tcc cag gtg gtc cat aag gct gtg ctt gat gta ttt gag 1166
Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu
      330                335                340
gag ggc aca gaa gca tct gct gcc aca gca gtc aaa atc acc ctc ctt 1214
Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu
      345                350                355                360
tct gca tta gtg gag aca agg acc att gtg cgt ttc aac agg ccc ttc 1262
Ser Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe
      365                370                375
ctg atg atc att gtc cct aca gac acc cag aac atc ttc ttc atg agc 1310
Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser
      380                385                390
aaa gtc acc aat ccc aag caa gcc tagagcttgc catcaagcag tggggctctc 1364
Lys Val Thr Asn Pro Lys Gln Ala
      395                400
agtaaggaac ttggaatgca agctggatgc ctgggtctct gggcacagcc tggcccctgt 1424
gcaccgagtg gccatggcat gtgtggccct gtctgcttat ccttggaagg tgacagcgat 1484
tcctctgtga gctctcacat gcacaggggc ccatggactc ttcagtctgg agggctcctgg 1544
gcctcctgac agcaataaat aatttcgttg gacacgcaaa aaaaaaaaaa aaa 1597

```

<210> 14  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

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<400> 14
Met Glu Arg Met Leu Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala Gly
      -20                -15                -10
Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
      -5                1                5
Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
      10                15                20                25
Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln Leu
      30                35                40
Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
      45                50                55
Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
      60                65                70
Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
      75                80                85
Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln
      90                95                100                105
Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
      110                115                120
Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
      125                130                135
Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
      140                145                150
Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile

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      155              160              165
Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
170              175              180              185
Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
      190              195              200
Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met
      205              210              215
Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
      220              225              230
Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
      235              240              245
Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
250              255              260              265
Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
      270              275              280
Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
      285              290              295
Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
      300              305              310
Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu
      315              320              325
Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu
330              335              340              345
Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser
      350              355              360
Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu
      365              370              375
Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys
      380              385              390
Val Thr Asn Pro Lys Gln Ala
      395              400

```

```

<210> 15
<211> 1397
<212> DNA
<213> Homo sapiens

```

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<220>
<221> 5'UTR
<222> 1..152

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<220>
<221> CDS
<222> 153..806

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<220>
<221> 3'UTR
<222> 807..1397

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<220>
<221> polyA_signal
<222> 1362..1367

```

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<220>
<221> polyA_site

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&lt;222&gt; 1382..1397

&lt;400&gt; 15

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agacctagga ggtgcgacag acccgcgggg caaacggact ggggcccaaga gccgggagcg 60
cgggcgcaaa ggcaccaggg cccgcccagg gcgcctcgca gcacggcctt gggggttctg 120
cgggccttcg ggtgcgcgtc tcgcctctag cc atg ggg tcc gca gcg ttg gag 173
                               Met Gly Ser Ala Ala Leu Glu
                               1 5
atc ctg ggc ctg gtg ctg tgc ctg gtg ggc tgg ggg ggt ctg atc ctg 221
Ile Leu Gly Leu Val Leu Cys Leu Val Gly Trp Gly Gly Leu Ile Leu
10 15 20
gcg tgc ggg ctg ccc atg tgg cag gtg acc gcc ttc ctg gac cac aac 269
Ala Cys Gly Leu Pro Met Trp Gln Val Thr Ala Phe Leu Asp His Asn
25 30 35
atc gtg acg gcg cag acc acc tgg aag ggg ctg tgg atg tgc tgc gtg 317
Ile Val Thr Ala Gln Thr Thr Trp Lys Gly Leu Trp Met Ser Cys Val
40 45 50 55
gtg cag agc acc ggg cac atg cag tgc aaa gtg tac gac tgc gtg ctg 365
Val Gln Ser Thr Gly His Met Gln Cys Lys Val Tyr Asp Ser Val Leu
60 65 70
gct ctg agc acc gag gtg cag gcg gcg gcg ctc acc gtg agc gcc 413
Ala Leu Ser Thr Glu Val Gln Ala Ala Arg Ala Leu Thr Val Ser Ala
75 80 85
gtg ctg ctg gcg ttc gtt gcg ctc ttc gtg acc ctg gcg ggc gcg cag 461
Val Leu Leu Ala Phe Val Ala Leu Phe Val Thr Leu Ala Gly Ala Gln
90 95 100
tgc acc acc tgc gtg gcc ccg ggc ccg gcc aag gcg cgt gtg gcc ctc 509
Cys Thr Thr Cys Val Ala Pro Gly Pro Ala Lys Ala Arg Val Ala Leu
105 110 115
acg gga ggc gtg ctc tac ctg ttt tgc ggg ctg ctg gcg ctc gtg cca 557
Thr Gly Gly Val Leu Tyr Leu Phe Cys Gly Leu Leu Ala Leu Val Pro
120 125 130 135
ctc tgc tgg ttc gcc aac att gtc gtc cgc gag ttt tac gac ccg tct 605
Leu Cys Trp Phe Ala Asn Ile Val Val Arg Glu Phe Tyr Asp Pro Ser
140 145 150
gtg ccc gtg tgc cag aag tac gag ctg ggc gca gcg ctg tac atc ggc 653
Val Pro Val Ser Gln Lys Tyr Glu Leu Gly Ala Ala Leu Tyr Ile Gly
155 160 165
tgg gcg gcc acc gcg ctg ctc atg gta ggc ggc tgc ctc ttg tgc tgc 701
Trp Ala Ala Thr Ala Leu Leu Met Val Gly Gly Cys Leu Leu Cys Cys
170 175 180
ggc gcc tgg gtc tgc acc ggc cgt ccc gac ctc agc ttc ccc gtg aag 749
Gly Ala Trp Val Cys Thr Gly Arg Pro Asp Leu Ser Phe Pro Val Lys
185 190 195
tac tca gcg ccg cgg cgg ccc acg gcc acc ggc gac aac gac aag aag 797
Tyr Ser Ala Pro Arg Arg Pro Thr Ala Thr Gly Asp Asn Asp Lys Lys
200 205 210 215
aac tac gtc tgagggcgct gggcacggcc gggcccctcc tgccagccac 846
Asn Tyr Val
gcctgcgagg cgttggataa gcctggggag ccccgcatgg accgcggtt ccgcccggta 906
gcgcggcgcg caggcttctc ggaacgtccg gctctgcgcc ccgacgcggc tcctggatcc 966
gctcctgcct gcgcccgcag ctgaccttct cctgccacta gcccggccct gcccttaaca 1026
gacggaatga agtttctttt tctgtgcgcg gcgctgtttc cataggcaga gcgggtgtca 1086
gactgaggat ttcgcttccc ctccaagacg ctgggggtct tggtgtgtgc cttacttccc 1146
agaggctcct gctgacttcg gaggggcgga tgcagagccc agggcccca ccggaagatg 1206

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tgtacagctg gtctttactc catcggcagg gcccgagccc agggaccagt gacttggcct 1266  
 ggacctcccg gtctcactcc agcatctccc caggcaaggc ttgtgggcac cggagcttga 1326  
 gagagggcgg gagtgggaag gctaagaatc tgcttagtaa atgggttgaa ctctgaaaaa 1386  
 aaaaaaaaaa a 1397

<210> 16  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Gly Ser Ala Ala Leu Glu Ile Leu Gly Leu Val Leu Cys Leu Val  
 1 5 10 15  
 Gly Trp Gly Gly Leu Ile Leu Ala Cys Gly Leu Pro Met Trp Gln Val  
 20 25 30  
 Thr Ala Phe Leu Asp His Asn Ile Val Thr Ala Gln Thr Thr Trp Lys  
 35 40 45  
 Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly His Met Gln Cys  
 50 55 60  
 Lys Val Tyr Asp Ser Val Leu Ala Leu Ser Thr Glu Val Gln Ala Ala  
 65 70 75 80  
 Arg Ala Leu Thr Val Ser Ala Val Leu Leu Ala Phe Val Ala Leu Phe  
 85 90 95  
 Val Thr Leu Ala Gly Ala Gln Cys Thr Thr Cys Val Ala Pro Gly Pro  
 100 105 110  
 Ala Lys Ala Arg Val Ala Leu Thr Gly Gly Val Leu Tyr Leu Phe Cys  
 115 120 125  
 Gly Leu Leu Ala Leu Val Pro Leu Cys Trp Phe Ala Asn Ile Val Val  
 130 135 140  
 Arg Glu Phe Tyr Asp Pro Ser Val Pro Val Ser Gln Lys Tyr Glu Leu  
 145 150 155 160  
 Gly Ala Ala Leu Tyr Ile Gly Trp Ala Ala Thr Ala Leu Leu Met Val  
 165 170 175  
 Gly Gly Cys Leu Leu Cys Cys Gly Ala Trp Val Cys Thr Gly Arg Pro  
 180 185 190  
 Asp Leu Ser Phe Pro Val Lys Tyr Ser Ala Pro Arg Arg Pro Thr Ala  
 195 200 205  
 Thr Gly Asp Asn Asp Lys Lys Asn Tyr Val  
 210 215

<210> 17  
 <211> 782  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..62

<220>  
 <221> CDS  
 <222> 63..572

<220>  
 <221> 3'UTR

<222> 573..782

<220>

<221> polyA\_signal

<222> 750..755

<220>

<221> polyA\_site

<222> 767..782

<400> 17

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atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
  Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
    1          5          10          15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
          20          25          30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
          35          40          45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
          50          55          60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
          65          70          75
ctt ggc ctc tat gct gat cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val
          80          85          90          95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
          100          105          110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
          115          120          125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
          130          135          140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
          145          150          155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
          160          165          170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt 652
caccccaatg ggaccacct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaaaaaa 772
aaaaaaaaaa 782

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<210> 18

<211> 170

<212> PRT

<213> Homo sapiens

```

<400> 18
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1          5          10          15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20          25          30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35          40          45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50          55          60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65          70          75          80
Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85          90          95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100         105         110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115         120         125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130         135         140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145         150         155         160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165         170

```

```

<210> 19
<211> 789
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..62

<220>
<221> CDS
<222> 63..572

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<220>
<221> 3'UTR
<222> 573..789

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<220>
<221> polyA_signal
<222> 750..755

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<220>
<221> polyA_site
<222> 774..789

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<400> 19
atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1          5          10          15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155

```



```

Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys
      20      25      30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
      35      40      45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
      50      55      60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
      65      70      75
ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
      80      85      90      95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
      100      105      110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
      115      120      125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
      130      135      140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
      145      150      155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
      160      165      170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
caccccaatg ggaccacct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
caaaaaaaaaa aaaaaaa 789

```

&lt;210&gt; 20

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

```

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1      5      10      15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys Glu
      20      25      30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
      35      40      45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
      50      55      60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
      65      70      75      80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
      85      90      95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
      100      105      110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn

```

<400> 21																	
aaaaacttta cggcaggcgt ccgcgtcgct agctagtcgt tctgaagcgg cggccagaga																	60
agagtcaagg gcacgagcat cggcc atg cct ttc ttg gac atc cag aaa agg																	112
Met Pro Phe Leu Asp Ile Gln Lys Arg																	
1 5																	
ttc ggc ctt aac ata gat cga tgg ttg aca atc cag agt tgt gaa cag																	160
Phe Gly Leu Asn Ile Asp Arg Trp Leu Thr Ile Gln Ser Cys Glu Gln																	
10 15 20 25																	
ccc tac aag atg gct ggt cga tgc cat gct ttt gaa aaa gaa tgg ata																	208
Pro Tyr Lys Met Ala Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile																	
30 35 40																	
gaa tgt gca cat gga atc ggt tat act cgg gca gag aaa gag tgc aag																	256
Glu Cys Ala His Gly Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys																	
45 50 55																	
ata gaa tat gat gat ttc gta gag tgt ttg ctt cgg cag aaa acg atg																	304
Ile Glu Tyr Asp Asp Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met																	
60 65 70																	
aga cgt gca ggt acc atc agg aag cag cgg gat aag ctg ata aag gaa																	352
Arg Arg Ala Gly Thr Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu																	
75 80 85																	
gga aag tac acc cct cca cct cac cac att ggc aag ggg gag cct tgg																	400
Gly Lys Tyr Thr Pro Pro Pro His His Ile Gly Lys Gly Glu Pro Trp																	

```

90          95          100          105
ccc tgaacagagc agctgctgat gtctggaggc tgattttcct gttctctggt 453
Pro
ctccactgga aaggttggtt acgacaaacc tccttggtcaa agtgtgtata aataaaggat 513
tgctccatcc tatttggtct attttcaaaa aaaaaaaaaa aa 555

```

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<210> 22
<211> 106
<212> PRT
<213> Homo sapiens

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<400> 22
Met Pro Phe Leu Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile Asp Arg
1          5          10          15
Trp Leu Thr Ile Gln Ser Cys Glu Gln Pro Tyr Lys Met Ala Gly Arg
          20          25          30
Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
          35          40          45
Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp Phe Val
          50          55          60
Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr Ile Arg
65          70          75          80
Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
          85          90          95
His His Ile Gly Lys Gly Glu Pro Trp Pro
          100          105

```

```

<210> 23
<211> 1726
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..414

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<220>
<221> CDS
<222> 415..1653

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<220>
<221> 3'UTR
<222> 1654..1726

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<220>
<221> polyA_site
<222> 1688..1726

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<400> 23
ctctccgcgc gccccctgca gccctggacg cagcacctcc gtttgggacg ccctacgccc 60
accttaactt gaggtcccca tccacgcagc ctctgcaagc ctcaccgcaa ccgtgctagg 120
cgcgtcgggt ggggcgggaa taaagttttt ccaaccaggt ttggggagag ggctggatgg 180
gaaggaccct ccctgctgca gacttcatgg caggctgcac tgtgtcccct cggctccacg 240
gctgccccgy gggcgctgct ttcgggtttt ctttctagaa tctctggtct gctgctgtgc 300
agatggacct gccggcactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360

```

```

gaggatgaag ttgaaattct gggacctttc cctgctcaga cccctccctg gctg atg 417
                                Met
                                1
gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465
Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser
                                5                                10                                15
gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513
Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser
                                20                                25                                30
tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561
Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser
                                35                                40                                45
agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609
Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro
50                                55                                60                                65
atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657
Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser
                                70                                75                                80
gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705
Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu
85                                90                                95
ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753
Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu
100                                105                                110
aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801
Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe
115                                120                                125
agc act cag tac gac ctg ctg cac aac cac ctc acc gtg cgc gtg atc 849
Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val Ile
130                                135                                140                                145
gag gcc agg gac ctg cca cct ccc atc tcc cac gat ggc tcg cgc cag 897
Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln
150                                155                                160
gac atg gcg cac tcc aac ccc tac gtc aag atc tgt ctc ctg cca gac 945
Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp
165                                170                                175
cag aag aac tca aag cag acc ggg gtc aaa cgc aag acc cag aag ccc 993
Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro
180                                185                                190
gtg ttt gag gag cgc tac acc ttc gag atc ccc ttc ctg gag gcc cag 1041
Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln
195                                200                                205
agg agg acc ctg ctc ctg acc gtg gtg gat ttt gat aag ttc tcc cgc 1089
Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg
210                                215                                220                                225
cac tgt gtc att ggg aaa gtt tct gtg cct ttg tgt gaa gtt gac ctg 1137
His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp Leu
230                                235                                240
gtc aag ggc ggg cac tgg tgg aag gcg ctg att ccc agt tct cag aat 1185
Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln Asn
245                                250                                255
gaa gtg gag ctg ggg gag ctg ctt ctg tca ctg aat tat ctc cca agt 1233
Glu Val Glu Leu Gly Glu Leu Leu Leu Ser Leu Asn Tyr Leu Pro Ser
260                                265                                270
gct ggc aga ctg aat gtt gat gtc att cga gcc aag caa ctt ctt cag 1281

```

```

Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln
 275                280                285
aca gat gtg agc caa ggt tca gac ccc ttt gtg aaa atc cag ctg gtg 1329
Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val
290                295                300                305
cat gga ctc aaa ctt gtg aaa acc aag aag acg tcc ttc tta agg ggc 1377
His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly
                310                315                320
aca att gat cct ttc tac aat gaa tcc ttc agc ttc aaa gtt ccc caa 1425
Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln
                325                330                335
gaa gaa ctg gaa aat gcc agc cta gtg ttt aca gtt ttc ggc cac aac 1473
Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn
                340                345                350
atg aag agc agc aat gac ttc atc ggg agg atc gtc att ggc cag tac 1521
Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr
                355                360                365
tct tca ggc ccc tct gag acc aac cac tgg agg cgc atg ctc aac acg 1569
Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr
370                375                380                385
cac cgc aca gcc gtg gag cag tgg cat agc ctg agg tcc cga gct gag 1617
His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu
                390                395                400
tgt gac cgc gtg tct cct gcc tcc ctg gag gtg acc tgagggctgc 1663
Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr
                405                410
aggggaaggca gctttcattt gtttaaaaaa aaaaaaaaaa aaagacgaaa aaaaaaaaaa 1723
aaa 1726

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<210> 24  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

```

<400> 24
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Ser Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg
                20                25                30
Ser Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile
                35                40                45
Ser Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys
                50                55                60
Pro Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro
65                70                75                80
Ser Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe
                85                90                95
Glu Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser
                100                105                110
Leu Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His
                115                120                125
Phe Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val
                130                135                140
Ile Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg
145                150                155                160

```

```

Gln Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro
      165      170      175
Asp Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys
      180      185      190
Pro Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala
      195      200      205
Gln Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser
      210      215      220
Arg His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp
225      230      235      240
Leu Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln
      245      250      255
Asn Glu Val Glu Leu Gly Glu Leu Leu Leu Ser Leu Asn Tyr Leu Pro
      260      265      270
Ser Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu
      275      280      285
Gln Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu
      290      295      300
Val His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg
305      310      315      320
Gly Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro
      325      330      335
Gln Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His
      340      345      350
Asn Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln
      355      360      365
Tyr Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn
      370      375      380
Thr His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala
385      390      395      400
Glu Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr
      405      410

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<210> 25  
 <211> 941  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..75

<220>  
 <221> CDS  
 <222> 76..339

<220>  
 <221> 3'UTR  
 <222> 340..941

<220>  
 <221> polyA\_signal  
 <222> 903..908

<220>

&lt;221&gt; polyA\_site

&lt;222&gt; 926..941

&lt;400&gt; 25

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agaaagccgc gcacctctc ccgccaggcg ctttctcgga cgccttgccc agcgggcccgc 60
ccgacccccct gcacc atg gac ccc gct cgc ccc ctg ggg ctg tcg att ctg 111
      Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu
                    -20                    -15
ctg ctt ttc ctg acg gag gct gca ctg ggc gat gct gct cag gag cca 159
Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro
      -10                    -5                    1
aca gga aat aac gcg gag atc tgt ctc ctg ccc cta gac tac gga ccc 207
Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro
5      10      15      20
tgc cgg gcc cta ctt ctc cgt tac tac tac gac agg tac acg cag agc 255
Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser
      25      30      35
tgc cgc cag ttc ctg tac ggg ggc tgc gag ggc aac gcc aac aat ttc 303
Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe
      40      45      50
tac acc tgg gag gct tgc gac gat ctt gct gga gga tagaaaaagt 349
Tyr Thr Trp Glu Ala Cys Asp Asp Leu Ala Gly Gly
      55      60
tcccaaagtt tgccggctgc aagtgagtgt ggacgaccag tgtgaggggt ccacagaaaa 409
gtattttcttt aatctaagtt ccatgacatg tgaaaaattc ttttccggtg ggtgtcaccg 469
gaaccggatt gagaacaggt ttccagatga agctacttgt atgggcttct gcgcaccaaa 529
gaaaattcca tcatttttgc acagtccaaa agatggggac tgtgctctgc caatgtgact 589
cgctattatt ttaatccaag atacagaacc tgtgatgctt tcacctatac tggctgtgga 649
gggaatgaca ataactttgt tagcagggag gattgcaaac gtgcatgtgc aaaagctttg 709
aaaaagaaaa agaagatgcc aaagcttcgc tttgccagta gaatccggaa aattcgggaag 769
aagcaatttt aaacattctt aatatgtcat cttgtttgtc tttatggctt atttgccttt 829
atggttgat ctgaagaata atatgacagc atgaggaaac aaatcattgg tgatttatcc 889
accagttttt attaatacaa gtcacttttt aaaaataaaa aaaaaaaaaa aa 941

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&lt;210&gt; 26

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..24

&lt;400&gt; 26

```

Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
      -20                    -15                    -10
Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
      -5                    1                    5
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
      10      15      20
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
25      30      35      40
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
      45      50      55
Ala Cys Asp Asp Leu Ala Gly Gly

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<210> 27
<211> 1894
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 21..1118
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<220>
<221> polyA_signal
<222> 1858..1863
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<400>	27																						
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												Met	Ala	Ser	Met	Ala	Ala	Val	Leu	Thr	Trp	Ala	
												-20				-15							
ctg	gct	ctt	ctt	tca	gcg	ttt	tcg	gcc	acc	cag	gca	cgg	aaa	ggc	ttc	101							
Leu	Ala	Leu	Leu	Ser	Ala	Phe	Ser	Ala	Thr	Gln	Ala	Arg	Lys	Gly	Phe								
				-10					-5					1									
tgg	gac	tac	ttc	agc	cag	acc	agc	ggg	gac	aaa	ggc	agg	gtg	gag	cag	149							
Trp	Asp	Tyr	Phe	Ser	Gln	Thr	Ser	Gly	Asp	Lys	Gly	Arg	Val	Glu	Gln								
5					10					15					20								
atc	cat	cag	cag	aag	atg	gct	cgc	gag	ccc	gcg	acc	ctg	aaa	gac	agc	197							
Ile	His	Gln	Gln	Lys	Met	Ala	Arg	Glu	Pro	Ala	Thr	Leu	Lys	Asp	Ser								
				25					30					35									
ctt	gag	caa	gac	ctc	aac	aat	atg	aac	aag	ttc	ctg	gaa	aag	ctg	agg	245							
Leu	Glu	Gln	Asp	Leu	Asn	Asn	Met	Asn	Lys	Phe	Leu	Glu	Lys	Leu	Arg								
				40					45					50									
cct	ctg	agt	ggg	agc	gag	gct	cct	cgg	ctc	cca	cag	gac	ccg	gtg	ggc	293							
Pro	Leu	Ser	Gly	Ser	Glu	Ala	Pro	Arg	Leu	Pro	Gln	Asp	Pro	Val	Gly								
				55					60					65									
atg	cgg	cgg	cag	ctg	cag	gag	gag	ttg	gag	gag	gtg	aag	gct	cgc	ctc	341							
Met	Arg	Arg	Gln	Leu	Gln	Glu	Glu	Leu	Glu	Glu	Val	Lys	Ala	Arg	Leu								
				70					75					80									
cag	ccc	tac	atg	gca	gag	gcg	cac	gag	ctg	gtg	ggc	tgg	aat	ttg	gag	389							
Gln	Pro	Tyr	Met	Ala	Glu	Ala	His	Glu	Leu	Val	Gly	Trp	Asn	Leu	Glu								
85					90					95					100								
ggc	ttg	cgg	cag	caa	ctg	aag	ccc	tac	acg	atg	gat	ctg	atg	gag	cag	437							
Gly	Leu	Arg	Gln	Gln	Leu	Lys	Pro	Tyr	Thr	Met	Asp	Leu	Met	Glu	Gln								
				105					110					115									



```

gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg 485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly
120 125 130
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct 533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala
135 140 145
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc 581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe
150 155 160
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg 629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly
165 170 175 180
cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc 677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala
185 190 195
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc 725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu
200 205 210
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac 773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp
215 220 225
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag 821
Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu
230 235 240
gaa ggg gcc ggc ccg gac ccc cag atg ctc tcc gag gag gtg cgc cag 869
Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln
245 250 255 260
cga ctt cag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc 917
Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe
265 270 275
act cgc gcc atc gac cag gag act gag gag gtc cag cag cag ctg gcg 965
Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala
280 285 290
cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca 1013
Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr
295 300 305
gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg 1061
Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu
310 315 320
tgg gaa gac atc act cac ctt cat gac cag ggc cac agc cat ctg 1109
Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu
325 330 335 340
ggg gac ccc tgaggatcta cctgccagg cccattccca gcttcttgtc 1158
Gly Asp Pro
tggggagcct tggctctgag cctctagcat gggttcagtc ttgaaagtgg cctgttgggt 1218
ggagggtgga aggtcctgtg caggacaggg aggccaccaa aggggctgct gtctcctgca 1278
tatccagcct cctgcgactc cccaatctgg atgcattaca ttcaccaggc tttgcaaacc 1338
cagcctccca gtgctcattt gggaatgctc atgagttact ccattcaagg gtgagggagt 1398
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cactgctaca gctggtccac agagaggagc acttgctctc ccagggctgc catggcagct 1578
atcaggggaa tagaaggag aaagagaata tcatggggag aacatgtgat ggtgtgtgaa 1638
tatccttctgct ggctctgatg ctggtgggta cgaaaggtgt gggctgtgat aggagagggc 1698
agagcccatg tttcctgaca tagctctaca cctaaataag ggactgaacc ctcccaactg 1758
tgggagctcc ttaaaccctc tggggagcat actgtgtgct ctccccatct ccagccctc 1818

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cctctggggtt cccaagttga agcctagact tctgggtcaa atgaaataga tgtttatgat 1878  
 aaaaaaaaaa aaaaaa 1894

<210> 28  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 28  
 Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser  
                   -20                  -15                  -10  
 Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser  
           -5                          1                          5  
 Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys  
 10                  15                  20                  25  
 Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu  
                   30                  35                  40  
 Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser  
           45                  50                  55  
 Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu  
           60                  65                  70  
 Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala  
           75                  80                  85  
 Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln  
 90                  95                  100                  105  
 Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val  
                   110                  115                  120  
 Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala  
                   125                  130                  135  
 Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu  
           140                  145                  150  
 Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His  
           155                  160                  165  
 Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu  
 170                  175                  180                  185  
 Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu  
                   190                  195                  200  
 Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys  
           205                  210                  215  
 Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu  
           220                  225                  230  
 Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro  
           235                  240                  245  
 Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe  
 250                  255                  260                  265  
 Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp  
                   270                  275                  280  
 Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly  
           285                  290                  295  
 His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val  
           300                  305                  310

Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr  
 315 320 325  
 His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro  
 330 335 340

<210> 29  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..31

<220>  
 <221> CDS  
 <222> 32..559

<220>  
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 <222> 560..742

<220>  
 <221> polyA\_signal  
 <222> 702..707

<220>  
 <221> polyA\_site  
 <222> 728..742

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 Met Thr Ser Gly Ser Lys Cys  
 1 5  
 cct agt aca gac tca gga aaa gaa gaa tat att gcc acg ttc aaa gga 100  
 Pro Ser Thr Asp Ser Gly Lys Glu Glu Tyr Ile Ala Thr Phe Lys Gly  
 10 15 20  
 tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att caa agc agc 148  
 Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile Gln Ser Ser  
 25 30 35  
 agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg aat gga ctg 196  
 Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg Asn Gly Leu  
 40 45 50 55  
 atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt gcc ctg aaa 244  
 Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu Ala Leu Lys  
 60 65 70  
 aat gga gct gtc tct ctg gtc att aat ttg gga tca ggg gcc ttt gaa 292  
 Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly Ala Phe Glu  
 75 80 85  
 gca cta gtg gag cct gtg aat gga aag ttt aat gat aat gcc tgg cat 340  
 Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn Ala Trp His  
 90 95 100  
 gat gtg aaa gtc acc agg aat ctg cgt cag gtg aca ata tca gtg gat 388  
 Asp Val Lys Val Thr Arg Asn Leu Arg Gln Val Thr Ile Ser Val Asp  
 105 110 115

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ggg att ctt acc aca acg ggc tac acg caa gaa gat tat acc atg ctg 436
Gly Ile Leu Thr Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu
120 125 130 135
ggg tct gat gac ttt ttc tat gtt gga ggc agt ccc agc aca gcc gac 484
Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp
140 145 150
ctt cca ggg tca cca atc cag cat gaa agc acc ttt gct gaa gac ccg 532
Leu Pro Gly Ser Pro Ile Gln His Glu Ser Thr Phe Ala Glu Asp Pro
155 160 165
atg ttc cag agt caa acg gca caa ctt taaattcaat attctactat 579
Met Phe Gln Ser Gln Thr Ala Gln Leu
170 175
tgtttatgta ggattggggg agggaaacag ctcatagatc attatgaagg aattaggttc 639
ctcttcttta ttagtctgta agtaatttac atttgagatt tgtgtggaca gttgatatta 699
gctataaaaag aaagtcaaac aaaaagagaa aaaaaaaaaa aaa 742

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<210> 30  
 <211> 176  
 <212> PRT  
 <213> Homo sapiens

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<400> 30
Met Thr Ser Gly Ser Lys Cys Pro Ser Thr Asp Ser Gly Lys Glu Glu
1 5 10 15
Tyr Ile Ala Thr Phe Lys Gly Ser Glu Tyr Phe Cys Tyr Asp Leu Ser
20 25 30
Gln Asn Pro Ile Gln Ser Ser Ser Asp Glu Ile Thr Leu Ser Phe Lys
35 40 45
Thr Leu Gln Arg Asn Gly Leu Met Leu His Thr Gly Lys Ser Ala Asp
50 55 60
Tyr Val Asn Leu Ala Leu Lys Asn Gly Ala Val Ser Leu Val Ile Asn
65 70 75 80
Leu Gly Ser Gly Ala Phe Glu Ala Leu Val Glu Pro Val Asn Gly Lys
85 90 95
Phe Asn Asp Asn Ala Trp His Asp Val Lys Val Thr Arg Asn Leu Arg
100 105 110
Gln Val Thr Ile Ser Val Asp Gly Ile Leu Thr Thr Thr Gly Tyr Thr
115 120 125
Gln Glu Asp Tyr Thr Met Leu Gly Ser Asp Asp Phe Phe Tyr Val Gly
130 135 140
Gly Ser Pro Ser Thr Ala Asp Leu Pro Gly Ser Pro Ile Gln His Glu
145 150 155 160
Ser Thr Phe Ala Glu Asp Pro Met Phe Gln Ser Gln Thr Ala Gln Leu
165 170 175

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<210> 31  
 <211> 1766  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..3

<220>

&lt;221&gt; CDS

&lt;222&gt; 4..1533

&lt;220&gt;

&lt;221&gt; 3'UTR

&lt;222&gt; 1534..1756

&lt;220&gt;

&lt;221&gt; polyA\_signal

&lt;222&gt; 1709..1714

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1744..1766

&lt;400&gt; 31

aag atg gcg gcg gag ctg gtg gag gcc aaa aac atg gtg atg agt ttt	48
Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe	
1 5 10 15	
cga gtc tcc gac ctt cag atg ctc ctg ggt ttc gtg ggc cgg agt aag	96
Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys	
20 25 30	
agt gga ctg aag cac gag ctc gtc acc agg gcc ctc cag ctg gtg cag	144
Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln	
35 40 45	
ttt gac tgt acc cct gag ctg ttc aag aag atc aag gag ctg tac gag	192
Phe Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu	
50 55 60	
acc cgc tac gcc aag aag aac tcg gag cct gcc cca cag ccg cac cgg	240
Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg	
65 70 75	
ccc ctg gac ccc ctg acc atg cac tcc acc tac gac cgg gcc ggc gct	288
Pro Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala	
80 85 90 95	
gtg ccc agg act ccg ctg gca ggc ccc aat att gac tac ccc gtg ctc	336
Val Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu	
100 105 110	
tac gga aag tac tta aac gga ctg gga cgg ttg ccc gcc aag acc ctc	384
Tyr Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu	
115 120 125	
aag cca gaa gtc cgc ctg gtg aag ctg ccg ttc ttt aat atg ctg gac	432
Lys Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp	
130 135 140	
gag ctg ctg aag ccc acc gaa tta gtc cca cag aac aac gag aag ctt	480
Glu Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu	
145 150 155	
cag gag agc ccg tgc atc ttc gca ttg acg cca aga cag gtg gag ttg	528
Gln Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu	
160 165 170 175	
atc cgg aac tcc agg gaa ctg cag ccc gga gtt aaa gcc gtg cag gtc	576
Ile Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val	
180 185 190	
gtc ctg aga atc tgt tac tca gac acc agc tgc cct cag gag gac cag	624
Val Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln	
195 200 205	

tac ccg ccc aac atc gct gtg aag gtc aac cac agc tac tgc tcc gtc	672
Tyr Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val	
210 215 220	
ccg ggc tac tac ccc tcc aat aag ccc ggg gtg gag ccc aag agg ccg	720
Pro Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro	
225 230 235	
tgc cgc ccc atc aac ctc acc cac ctc atg tac ctt tcc tcg gcc acc	768
Cys Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr	
240 245 250 255	
aac cgc atc act gtc acc tgg ggg aac tac ggc aag agc tac tcg gtg	816
Asn Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val	
260 265 270	
gcc ctg tac ctg gtg cgg cag ctg acc tca tcg gag ctg ctg cag agg	864
Ala Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg	
275 280 285	
ctg aag acc att ggg gta aag cac ccg gag ctg tgc aag gca ctg gtc	912
Leu Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val	
290 295 300	
aag gag aag ctg cgc ctt gat cct gac agc gag atc gcc acc acc ggt	960
Lys Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly	
305 310 315	
gtg cgg gtg tcc ctc atc tgt ccg ctg gtg aag atg cgg ctc tcc gtg	1008
Val Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val	
320 325 330 335	
ccc tgc cgg gca gag acc tgc gcc cac ctg cag tgc ttc gac gcc gtc	1056
Pro Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val	
340 345 350	
ttc tac ctg cag atg aac gag aag aag ccc acc tgg atg tgc ccc gtg	1104
Phe Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val	
355 360 365	
tgc gac aag cca gcc ccc tac gac cag ctc atc atc gac ggg ctc ctc	1152
Cys Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu	
370 375 380	
tcg aag atc ctg agc gag tgt gag gac gcc gac gag atc gag tac ctg	1200
Ser Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu	
385 390 395	
gtg gac ggc tcg tgg tgc ccg atc cgc gcc gaa aag gag ctc agc tgc	1248
Val Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys	
400 405 410 415	
agc ccg cag ggc gcc atc ctc gtg ctg ggc ccc tcg gac gcc aat ggg	1296
Ser Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly	
420 425 430	
ctc ctg ccc gcc ccc agc gtc aac ggg agc ggt gcc ctg ggc agc acg	1344
Leu Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr	
435 440 445	
ggt ggc ggc ggc ccg gtg ggc agc atg gag aat ggg aag ccg ggc gcc	1392
Gly Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala	
450 455 460	
gat gtg gtg gac ctc acg ctg gac agc tca tcg tcc tcg gag gat gag	1440
Asp Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu	
465 470 475	
gag gag gag gaa gag gag gag gaa gac gag gac gaa gag ggg ccc ccg	1488
Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg	
480 485 490 495	
ccc aag cgc cgc tgc ccc ttc cag aag ggc ctg gtg ccg gcc tgc	1533

Pro Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys  
                   500                  505                  510  
 tgaccccggc cgcacacttg acttttcctgg tgctcaccac gcagaggggc acggggccagc 1593  
 ctcgggcgca gagggaggag tgacctttct ttttcctttt attgtcggtc gttttgtttt 1653  
 tccacccttt tgcttggtc ctggcacctg tacctctgga ctctcctatc gggggattaa 1713  
 aaaaaaagt aaaatgacaa aaaaagatac aaaaaagaaa aaaaaaaaaa aaa 1766

<210> 32  
 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg  
 1                  5                  10                  15  
 Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser  
                   20                  25                  30  
 Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe  
                   35                  40                  45  
 Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr  
                   50                  55                  60  
 Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro  
 65                  70                  75                  80  
 Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala Val  
                   85                  90                  95  
 Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu Tyr  
                   100                  105                  110  
 Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu Lys  
                   115                  120                  125  
 Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp Glu  
                   130                  135                  140  
 Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu Gln  
 145                  150                  155                  160  
 Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu Ile  
                   165                  170                  175  
 Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val Val  
                   180                  185                  190  
 Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln Tyr  
                   195                  200                  205  
 Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val Pro  
                   210                  215                  220  
 Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro Cys  
 225                  230                  235                  240  
 Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr Asn  
                   245                  250                  255  
 Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val Ala  
                   260                  265                  270  
 Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg Leu  
                   275                  280                  285  
 Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val Lys  
                   290                  295                  300  
 Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly Val  
 305                  310                  315                  320  
 Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val Pro  
                   325                  330                  335

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Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val Phe
      340      345      350
Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val Cys
      355      360      365
Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu Ser
      370      375      380
Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu Val
      385      390      395      400
Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys Ser
      405      410      415
Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly Leu
      420      425      430
Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr Gly
      435      440      445
Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala Asp
      450      455      460
Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu Glu
      465      470      475      480
Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro
      485      490      495
Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys
      500      505      510

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<210> 33
<211> 877
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..10

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<220>
<221> CDS
<222> 11..802

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<220>
<221> 3'UTR
<222> 803..877

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<220>
<221> polyA_signal
<222> 836..841

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<220>
<221> polyA_site
<222> 862..877

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<400> 33
atctgccacg atg ttg ctg ctc agc ctg acc cta agc ctg gtt ctc ctc      49
      Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu
      -15      -10
ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc      97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
-5      1      5      10

```



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ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg 145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
      15                20                25
ccc tgg cag gtg tcc ctg cag gac agc agc gac ttc cac ttc tgc ggt 193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly
      30                35                40
ggg tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat 241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
      45                50                55
gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca 289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
      60                65                70                75
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca 337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr
      80                85                90
cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg 385
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu
      95                100                105
aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc 433
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys
      110                115                120
ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc 481
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr
      125                130                135
acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cgt 529
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg
      140                145                150                155
ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag 577
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln
      160                165                170
tac tgg ggc tca agt atc act gac tcc atg atc tgt gca ggt ggc gca 625
Tyr Trp Gly Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala
      175                180                185
ggg gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag 673
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln
      190                195                200
aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa 721
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys
      205                210                215
aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc 769
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe
      220                225                230                235
agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc 822
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
      240                245
cccagctcaa cccattaaag acccaggccc tgtcccatca aaaaaaaaaa aaaaa 877

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<210> 34
<211> 264
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..18

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&lt;400&gt; 34

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Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
      -15                      -10                      -5
Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
      1                      5                      10
Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
15      20      25      30
Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly Gly Ser Leu
      35      40      45
Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
      50      55      60
Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
      65      70      75
Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
      80      85      90
Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
95      100      105      110
Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
      115      120      125
Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
      130      135      140
Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
      145      150      155
Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
      160      165      170
Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
175      180      185      190
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
      195      200      205
Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
      210      215      220
Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
      225      230      235
Ile Asn Gln Val Ile Ala Tyr Asn
      240      245

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&lt;210&gt; 35

&lt;211&gt; 1728

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 5'UTR

&lt;222&gt; 1..37

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 38..1378

&lt;220&gt;

&lt;221&gt; 3'UTR

&lt;222&gt; 1379..1728

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1713..1728

&lt;400&gt; 35

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atcatctgca cagctggggc ccctgggagg agacgcc atg atc ccc acc ttc acg      55
                               Met Ile Pro Thr Phe Thr
                               -20
gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag      103
Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln
      -15                               -10                               -5
gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg      151
Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val
      1                               5                               10                               15
atc agc tgg ggg aac tct gtg acc atc tgg tgt cag ggg acc ctg gag      199
Ile Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu
      20                               25                               30
gct cgg gag tac cgt ctg gat aaa gag gaa agc cca gca ccc tgg gac      247
Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp
      35                               40                               45
aga cag aac cca ctg gag ccc aag aac aag gcc aga ttc tcc atc cca      295
Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro
      50                               55                               60
tcc atg aca gag gac tat gca ggg aga tac cgc tgt tac tat cgc agc      343
Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser
      65                               70                               75
cct gta ggc tgg tca cag ccc agt gac ccc ctg gag ctg gtg atg aca      391
Pro Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr
      80                               85                               90                               95
gga gcc tac agt aaa ccc acc ctt tca gcc ctg ccg agt cct ctt gtg      439
Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val
      100                               105                               110
acc tca gaa aag agc gtg acc ctg ctg tgt cag tca cgg agc cca atg      487
Thr Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met
      115                               120                               125
gac act ttc ctt ctg atc aag gag cgg gca gcc cat ccc cta ctg cat      535
Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His
      130                               135                               140
ctg aga tca gag cac gga gct cag cag cac cag gct gaa ttc ccc atg      583
Leu Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met
      145                               150                               155
agt cct gtg acc tca gtg cac ggg ggg acc tac agg tgc ttc agc tca      631
Ser Pro Val Thr Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser
      160                               165                               170                               175
cac ggc ttc tcc cac tac ctg ctg tca cac ccc agt gac ccc ctg gag      679
His Gly Phe Ser His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu
      180                               185                               190
ctc ata gtc tca gga tcc ttg gag gat ccc agg ccc tca ccc aca agg      727
Leu Ile Val Ser Gly Ser Leu Glu Asp Pro Arg Pro Ser Pro Thr Arg
      195                               200                               205
tcc gtc tca aca gct gca ggc cct gag gac cag ccc ctc atg cct aca      775
Ser Val Ser Thr Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr
      210                               215                               220
ggg tca gtc ccc cac agt ggt ctg aga agg cac tgg gag gta ctg atc      823
Gly Ser Val Pro His Ser Gly Leu Arg Arg His Trp Glu Val Leu Ile
      225                               230                               235

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ggg gtc ttg gtg gtc tcc atc ctg ctt ctc tcc ctc ctc ttc ctc 871
Gly Val Leu Val Val Ser Ile Leu Leu Leu Ser Leu Leu Leu Phe Leu
240                245                250                255
ctc ctc caa cac tgg cgt cag gga aaa cac agg aca ttg gcc cag aga 919
Leu Leu Gln His Trp Arg Gln Gly Lys His Arg Thr Leu Ala Gln Arg
260                265                270
cag gct gat ttc caa cgt cct cca ggg gct gcc gag cca gag ccc aag 967
Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala Ala Glu Pro Glu Pro Lys
275                280                285
gac ggg ggc cta cag agg agg tcc agc cca gct gct gac gtc cag gga 1015
Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly
290                295                300
gaa aac ttc tgt gct gcc gtg aag gac aca cag cct gag gac ggg gtg 1063
Glu Asn Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val
305                310                315
gaa atg gac act cgg agc cca cac gat gaa gac ccc cag gca gtg acg 1111
Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr
320                325                330                335
tat gcc aag gtg aaa cac tcc aga cct agg aga gaa atg gcc tct cct 1159
Tyr Ala Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro
340                345                350
ccc tcc cca ctg tct ggg gaa ttc ctg gac aca aag gac aga cag gca 1207
Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala
355                360                365
gaa gag gac aga cag atg gac act gag gct gct gca tct gaa gcc ccc 1255
Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro
370                375                380
cag gat gtg acc tac gcc cag ctg cac agc ttt acc ctc aga cag aag 1303
Gln Asp Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys
385                390                395
gca act gag cct cct cca tcc cag gaa ggg gcc tct cca gct gag ccc 1351
Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro
400                405                410                415
agt gtc tat gcc act ctg gcc atc cac taatccaggg gggacccaga 1398
Ser Val Tyr Ala Thr Leu Ala Ile His
420
ccccacaagc catggagact caggacccca gaaggcatgg aagctgcctc cagtagacat 1458
cactgaaccc cagccagccc agaccctga cacagaccac tagaagattc cggaacggt 1518
gggagtcacc tgattctgca aagataaata atatccctgc attatcaaaa taaagtagca 1578
gacctctcaa ttcacaatga gttaactgat aaacaaaac agaagtcaga caatgtttta 1638
aattgaatga tcatgtaaat attacacatc aaaccaatga catgggaaaa tgggagcttc 1698
taatgaggac aaacaaaaaa aaaaaaaaaa 1728

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<210> 36  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 36  
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Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp  
 -5 1 5  
 Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp  
 10 15 20 25  
 Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu  
 30 35 40  
 Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys  
 45 50 55  
 Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr  
 60 65 70  
 Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro  
 75 80 85  
 Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala  
 90 95 100 105  
 Leu Pro Ser Pro Leu Val Thr Ser Glu Lys Ser Val Thr Leu Leu Cys  
 110 115 120  
 Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala  
 125 130 135  
 Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His  
 140 145 150  
 Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr  
 155 160 165  
 Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His  
 170 175 180 185  
 Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Asp Pro  
 190 195 200  
 Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp  
 205 210 215  
 Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg  
 220 225 230  
 His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu  
 235 240 245  
 Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His  
 250 255 260 265  
 Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala  
 270 275 280  
 Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro  
 285 290 295  
 Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asp Thr  
 300 305 310  
 Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu  
 315 320 325  
 Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro Arg  
 330 335 340 345  
 Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp  
 350 355 360  
 Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala  
 365 370 375  
 Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser  
 380 385 390  
 Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly  
 395 400 405  
 Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His  
 410 415 420

<210> 37  
 <211> 1757  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..329

<220>  
 <221> CDS  
 <222> 330..1478

<220>  
 <221> 3'UTR  
 <222> 1479..1757

<220>  
 <221> polyA\_signal  
 <222> 1722..1727

<220>  
 <221> polyA\_site  
 <222> 1742..1757

<400> 37  
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 cggccccctg cttgcgctcc cgaagaggag agcaaggctg ttctgggacg cggccgctcg 180  
 gcggcaagag gcttgtctgt ccgggttgcc ggaaccagga gaaccagag ggaaaccgag 240  
 gcaaaggagc ggcgcgtttt actagagaga gcgcgagcgg aagaggcgag agcaggagcg 300  
 cgcgagggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc 353  
 Met Arg Thr Tyr Trp Leu His Ser  
 -20  
 gtc tgg gtg ctg ggc ttt ttc ctg tcc ctc ttc tca ttg caa gga ctg 401  
 Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu  
 -15 -10 -5 1  
 cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg 449  
 Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val  
 5 10 15  
 agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac 497  
 Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn  
 20 25 30  
 tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat 545  
 Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His  
 35 40 45  
 gac aag tgg tct ctg gac cca cgg gtt gag ctg gag aaa cgc cat tct 593  
 Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser  
 50 55 60 65  
 ctg gaa tac agc ctc cga atc cag aag gtg gat gtc tat gat gag ggt 641  
 Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly  
 70 75 80  
 tcc tac act tgc tca gtt cag aca cag cat gag ccc aag acc tcc caa 689  
 Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln  
 85 90 95

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gtt tac ttg atc gta caa gtc cca cca aag atc tcc aat atc tcc tcg 737
Val Tyr Leu Ile Val Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser
100 105 110
gat gtc act gtg aat gag ggc agc aac gtg act ctg gtc tgc atg gcc 785
Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala
115 120 125
aat ggc cgt cct gaa cct gtt atc acc tgg aga cac ctt aca cca act 833
Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr
130 135 140 145
gga agg gaa ttt gaa gga gaa gaa gaa tat ctg gag atc ctt ggc atc 881
Gly Arg Glu Phe Glu Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile
150 155 160
acc agg gag cag tca ggc aaa tat gag tgc aaa gct gcc aac gag gtc 929
Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val
165 170 175
tcc tcg gcg gat gtc aaa caa gtc aag gtc act gtg aac tat cct ccc 977
Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro
180 185 190
act atc aca gaa tcc aag agc aat gaa gcc acc aca gga cga caa gct 1025
Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala
195 200 205
tca ctc aaa tgt gag gcc tcg gca gtg cct gca cct gac ttt gag tgg 1073
Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp
210 215 220 225
tac cgg gat gac act agg ata aat agt gcc aat ggc ctt gag att aag 1121
Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys
230 235 240
agc acg gag ggc cag tct tcc ctg acg gtg acc aac gtc act gag gag 1169
Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu
245 250 255
cac tac ggc aac tac acc tgt gtg gct gcc aac aag ctg ggg gtc acc 1217
His Tyr Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr
260 265 270
aat gcc agc cta gtc ctt ttc aaa cgt gtt tta ccc aca atc ccc cac 1265
Asn Ala Ser Leu Val Leu Phe Lys Arg Val Leu Pro Thr Ile Pro His
275 280 285
ccc att caa gaa att ggt acc acc gtg cac ttc aag caa aaa ggc atc 1313
Pro Ile Gln Glu Ile Gly Thr Thr Val His Phe Lys Gln Lys Gly Ile
290 295 300 305
ttc ctc tct gag tct cag agg ggt gag aca acc aag atc act ctc aac 1361
Phe Leu Ser Glu Ser Gln Arg Gly Glu Thr Thr Lys Ile Thr Leu Asn
310 315 320
tgt gga aat cta ttc ttg cgg aac tta cat ccc acc agt gat caa gag 1409
Cys Gly Asn Leu Phe Leu Arg Asn Leu His Pro Thr Ser Asp Gln Glu
325 330 335
cca cag aga tta tgg aca ctt tgt tgc tta ctc cca aga aag ggc cag 1457
Pro Gln Arg Leu Trp Thr Leu Cys Cys Leu Leu Pro Arg Lys Gly Gln
340 345 350
cac cgt att tat ggc cag tgc tagaagggtcc tcaactgaagg caacagggaa 1508
His Arg Ile Tyr Gly Gln Cys
355 360
gaggcagcca tgaatatata cttggaaaca ggatcatttg aggccttcaa gaaggcataa 1568
aatattgtcc ctttcagcct ttcttttctt ctcaatgccg cgattaccaa ttatgtttta 1628
atcttaagtg gctagtgtta tatgtgatac attatgcctt tgatatgtgg ttgaaaaaat 1688
aaggcatagc attgtttttt atttcaaaga caaaataaac tgccagtgtc accaaaaaaa 1748

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aaaaaaaaa

1757

<210> 38  
 <211> 383  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 38  
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           -5                          1                  5  
 Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr Ala Ile Leu  
 10                  15                  20                  25  
 Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp Leu Asn Arg  
                   30                  35                  40  
 Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu Asp Pro Arg  
                   45                  50                  55  
 Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu Arg Ile Gln  
           60                  65                  70  
 Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser Val Gln Thr  
           75                  80                  85  
 Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val Gln Val Pro  
 90                  95                  100                  105  
 Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn Glu Gly Ser  
                   110                  115                  120  
 Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu Pro Val Ile  
                   125                  130                  135  
 Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu Gly Glu Glu  
           140                  145                  150  
 Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser Gly Lys Tyr  
           155                  160                  165  
 Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val Lys Gln Val  
 170                  175                  180                  185  
 Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser Lys Ser Asn  
                   190                  195                  200  
 Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu Ala Ser Ala  
                   205                  210                  215  
 Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr Arg Ile Asn  
           220                  225                  230  
 Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln Ser Ser Leu  
           235                  240                  245  
 Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val  
 250                  255                  260                  265  
 Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val Leu Phe Lys  
                   270                  275                  280  
 Arg Val Leu Pro Thr Ile Pro His Pro Ile Gln Glu Ile Gly Thr Thr  
           285                  290                  295  
 Val His Phe Lys Gln Lys Gly Ile Phe Leu Ser Glu Ser Gln Arg Gly  
           300                  305                  310  
 Glu Thr Thr Lys Ile Thr Leu Asn Cys Gly Asn Leu Phe Leu Arg Asn



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      315              320              325
Leu His Pro Thr Ser Asp Gln Glu Pro Gln Arg Leu Trp Thr Leu Cys
330              335              340              345
Cys Leu Leu Pro Arg Lys Gly Gln His Arg Ile Tyr Gly Gln Cys
              350              355              360

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<210> 39
<211> 2818
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..80

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<220>
<221> CDS
<222> 81..1517

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<220>
<221> 3'UTR
<222> 1518..2818

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<220>
<221> polyA_signal
<222> 2786..2791

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<220>
<221> polyA_site
<222> 2804..2818

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<400> 39
ggcttttgggg cagggcagat ttatatctgc gggggatcag ctgacgctcc gcattgcaga 60
ctgcggagtc agacggcgct atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg 113
              Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu
              1              5              10
ggc gcg gct cta gcc ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg 161
Gly Ala Ala Leu Ala Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg
              15              20              25
ggc tcg gca gtg tgg tgc cag aat gtg aag acg gcg tcc gac tgc ggg 209
Gly Ser Ala Val Trp Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly
              30              35              40
gca gtg aag cac tgc ctg cag acc gtt tgg aac aag cca aca gtg aaa 257
Ala Val Lys His Cys Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys
              45              50              55
tcc ctt ccc tgc gac ata tgc aaa gac gtt gtc acc gca gct ggt gat 305
Ser Leu Pro Cys Asp Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp
60              65              70              75
atg ctg aag gac aat gcc act gag gag gag atc ctt gtt tac ttg gag 353
Met Leu Lys Asp Asn Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu
              80              85              90
aag acc tgt gac tgg ctt ccg aaa ccg aac atg tct gct tca tgc aag 401
Lys Thr Cys Asp Trp Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys
              95              100              105
gag ata gtg gac tcc tac ctc cct gtc atc ctg gac atc att aaa gga 449

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Glu	Ile	Val	Asp	Ser	Tyr	Leu	Pro	Val	Ile	Leu	Asp	Ile	Ile	Lys	Gly		
		110					115				120						
gaa	atg	agc	cgt	cct	ggg	gag	gtg	tgc	tct	gct	ctc	aac	ctc	tgc	gag	497	
Glu	Met	Ser	Arg	Pro	Gly	Glu	Val	Cys	Ser	Ala	Leu	Asn	Leu	Cys	Glu		
		125				130				135							
tct	ctc	cag	aag	cac	cta	gca	gag	ctg	aat	cac	cag	aag	cag	ctg	gag	545	
Ser	Leu	Gln	Lys	His	Leu	Ala	Glu	Leu	Asn	His	Gln	Lys	Gln	Leu	Glu		
		140			145					150					155		
tcc	aat	aag	atc	cca	gag	ctg	gac	atg	act	gag	gtg	gtg	gcc	ccc	ttc	593	
Ser	Asn	Lys	Ile	Pro	Glu	Leu	Asp	Met	Thr	Glu	Val	Val	Ala	Pro	Phe		
				160					165					170			
atg	gcc	aac	atc	cct	ctc	ctc	ctc	tac	cct	cag	gac	ggc	ccc	cgc	agc	641	
Met	Ala	Asn	Ile	Pro	Leu	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Arg	Ser		
				175				180					185				
aag	ccc	cag	cca	aag	gat	aat	ggg	gac	gtt	tgc	cag	gac	tgc	att	cag	689	
Lys	Pro	Gln	Pro	Lys	Asp	Asn	Gly	Asp	Val	Cys	Gln	Asp	Cys	Ile	Gln		
		190				195					200						
atg	gtg	act	gac	atc	cag	act	gct	gta	cgg	acc	aac	tcc	acc	ttt	gtc	737	
Met	Val	Thr	Asp	Ile	Gln	Thr	Ala	Val	Arg	Thr	Asn	Ser	Thr	Phe	Val		
		205				210					215						
cag	gcc	ttg	gtg	gaa	cat	gtc	aag	gag	gag	tgt	gac	cgc	ctg	ggc	cct	785	
Gln	Ala	Leu	Val	Glu	His	Val	Lys	Glu	Glu	Cys	Asp	Arg	Leu	Gly	Pro		
					225					230					235		
ggc	atg	gcc	gac	ata	tgc	aag	aac	tat	atc	agc	cag	tat	tct	gaa	att	833	
Gly	Met	Ala	Asp	Ile	Cys	Lys	Asn	Tyr	Ile	Ser	Gln	Tyr	Ser	Glu	Ile		
				240					245					250			
gct	atc	cag	atg	atg	atg	cac	atg	cag	gat	cag	caa	ccc	aag	gag	atc	881	
Ala	Ile	Gln	Met	Met	Met	His	Met	Gln	Asp	Gln	Gln	Pro	Lys	Glu	Ile		
				255				260						265			
tgt	gcg	ctg	gtt	ggg	ttc	tgt	gat	gag	gtg	aaa	gag	atg	ccc	atg	cag	929	
Cys	Ala	Leu	Val	Gly	Phe	Cys	Asp	Glu	Val	Lys	Glu	Met	Pro	Met	Gln		
		270					275					280					
act	ctg	gtc	ccc	gcc	aaa	gtg	gcc	tcc	aag	aat	gtc	atc	cct	gcc	ctg	977	
Thr	Leu	Val	Pro	Ala	Lys	Val	Ala	Ser	Lys	Asn	Val	Ile	Pro	Ala	Leu		
		285				290					295						
gaa	ctg	gtg	gag	ccc	att	aag	aag	cac	gag	gtc	cca	gca	aag	tct	gat	1025	
Glu	Leu	Val	Glu	Pro	Ile	Lys	Lys	His	Glu	Val	Pro	Ala	Lys	Ser	Asp		
				305						310					315		
gtt	tac	tgt	gag	gtg	tgt	gaa	ttc	ctg	gtg	aag	gag	gtg	acc	aag	ctg	1073	
Val	Tyr	Cys	Glu	Val	Cys	Glu	Phe	Leu	Val	Lys	Glu	Val	Thr	Lys	Leu		
				320						325				330			
att	gac	aac	aac	aag	act	gag	aaa	gaa	ata	ctc	gac	gct	ttt	gac	aaa	1121	
Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu	Ile	Leu	Asp	Ala	Phe	Asp	Lys		
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atg	tgc	tcg	aag	ctg	ccg	aag	tcc	ctg	tcg	gaa	gag	tgc	cag	gag	gtg	1169	
Met	Cys	Ser	Lys	Leu	Pro	Lys	Ser	Leu	Ser	Glu	Glu	Cys	Gln	Glu	Val		
				350			355					360					
gtg	gac	acg	tac	ggc	agc	tcc	atc	ctg	tcc	atc	ctg	ctg	gag	gag	gtc	1217	
Val	Asp	Thr	Tyr	Gly	Ser	Ser	Ile	Leu	Ser	Ile	Leu	Leu	Glu	Glu	Val		
				365			370				375						
agc	cct	gag	ctg	gtg	tgc	agc	atg	ctg	cac	ctc	tgc	tct	ggc	acg	cgg	1265	
Ser	Pro	Glu	Leu	Val	Cys	Ser	Met	Leu	His	Leu	Cys	Ser	Gly	Thr	Arg		
				380		385				390					395		
ctg	cct	gca	ctg	acc	gtt	cac	gtg	act	cag	cca	aag	gac	ggg	ggc	ttc	1313	
Leu	Pro	Ala	Leu	Thr	Val	His	Val	Thr	Gln	Pro	Lys	Asp	Gly	Gly	Phe		

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          400          405          410
tgc gaa gtg tgc aag aag ctg gtg ggt tat ttg gat cgc aac ctg gag 1361
Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu
          415          420          425
aaa aac agc acc aag cag gag atc ctg gct gct ctt gag aaa ggc tgc 1409
Lys Asn Ser Thr Lys Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys
          430          435          440
agc ttc ctg cca gac cct tac cag aag cag tgt gat cag ttt gtg gca 1457
Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala
          445          450          455
gag tac gag ccc gtg ctg atc gag atc ctg gtg gag gta tgg atc ctt 1505
Glu Tyr Glu Pro Val Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu
          460          465          470          475
cct tcg tgt gct tgaaaattgg agcctgcccc tcggcccata agcccttggt 1557
Pro Ser Cys Ala
gggaactgag aagtgtatat ggggcccagg ctactggtgc cagaacacag agacagcagc 1617
ccagtgcaat gctgtcgagc attgcaaagc ccatgtgtgg aactaggagg aggaatatcc 1677
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ttggaagctg tctgtggccc acttgggcac ccacgcttct gtccacttct ggttgccagg 2697
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ttttgcacta aagtttctgt gatttaacaa taaaattctg ttagccaaaa aaaaaaaaaa 2817
a 2818

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<210> 40  
 <211> 479  
 <212> PRT  
 <213> Homo sapiens

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<400> 40
Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1          5          10          15
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
          20          25          30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
          35          40          45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
          50          55          60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65          70          75          80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp

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<210> 41
<211> 770
<212> DNA
<213> Homo sapiens
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<220>  
 <221> 5'UTR  
 <222> 1..120

<220>  
 <221> CDS  
 <222> 121..546

<220>  
 <221> 3'UTR  
 <222> 547..770

<220>  
 <221> polyA\_signal  
 <222> 739..744

<220>  
 <221> polyA\_site  
 <222> 755..770

<400> 41  
 cttttcttgg gctctaagga cccaggagtc tgggtgcaca gcctccttct ctctgagatt 60  
 caagagtctg atcagcagcc tcttcctcct ccaggaccca gaagccctga gcttatcccc 120  
 atg gag ctc tgc cgg tcc ctg gcc ctg ctg ggg ggc tcc ctg ggc ctg 168  
 Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu  
 -35 -30 -25  
 atg ttc tgc ctg att gct ttg agc acc gat ttc tgg ttt gag gct gtg 216  
 Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val  
 -20 -15 -10  
 ggt ccc acc cac tca gct cac tcg ggc ctc tgg cca aca ggg cat ggg 264  
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly  
 -5 1 5 10  
 gac atc ata tca ggc cac ggc ccg ctt gtc tca acc acc gca gcc ttt 312  
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe  
 15 20 25  
 gct gca ggt aag gac tct gga ctg gac tgg ggc atc gcg agc cag cga 360  
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg  
 30 35 40  
 att cct gcc gag gag ctg agc cat ctc tct tgt cct tgt ccc cag cca 408  
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro  
 45 50 55  
 tct cca tgg tgg tgg cca tgg cgg tgt aca cca gcg agc ggt ggg acc 456  
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr  
 60 65 70 75  
 agc ctc cac acc ccc aga tcc aga cct tct tct cct ggt cct tct acc 504  
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr  
 80 85 90  
 tgg gct ggg tct cag cta tcc tct tgc tct gta cag gtg ccc 546  
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro  
 95 100 105  
 tgagcctggg tgctcactgt ggcggtcccc gtcttggtta tgaaaccttg tgagcagaag 606  
 gcaagagcgg caagatgagt tttgagcggt gtattccaaa ggccctcatct ggagcctcgg 666  
 gaaagtcttg tcccacatct gcccgccctt ccagcccttc cccagccctt cctcttgttt 726  
 cttcattcat tcaacaaaat ttggctggaa aaaaaaaaaa aaaa 770

<210> 42  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..37

<400> 42  
 Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu  
           -35                  -30                  -25  
 Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val  
           -20                  -15                  -10  
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly  
   -5                          1                  5                  10  
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe  
           15                  20                  25  
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg  
           30                  35                  40  
 Ile Prc Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro  
   45                          50                  55  
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr  
 60                          65                  70                  75  
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr  
                   80                  85                  90  
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro  
           95                  100                  105

<210> 43  
 <211> 1340  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..135

<220>  
 <221> CDS  
 <222> 136..501

<220>  
 <221> 3'UTR  
 <222> 502..1340

<220>  
 <221> polyA\_signal  
 <222> 1232..1237

<220>  
 <221> polyA\_site  
 <222> 1255..1340

<400> 43

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ctcttttggg gttcttcctt tctctctcag ctctccgtct ctctttctct ctcagcctct 60
ttctttctcc ctgtctcccc cactgtcagc acctcttctg tgtggtgagt ggaccgctta 120
ccccactagg tgaag atg tca gcc cag gag agc tgc ctc agc ctc atc aag 171
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys
      1      5      10
tac ttc ctc ttc gtt ttc aac ctc ttc ttc ttc gtc ctc ggc agc ctg 219
Tyr Phe Leu Phe Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu
      15      20      25
atc ttc tgc ttc ggc atc tgg atc ctc att gac aag acc agc ttc gtg 267
Ile Phe Cys Phe Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val
      30      35      40
tcc ttt gtg ggc ttg gcc ttc gtg cct ctg cag atc tgg tcc aaa gtc 315
Ser Phe Val Gly Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val
      45      50      55      60
ctg gcc atc tca gga atc ttc acc atg ggc atc gcc ctc ctg ggt tgt 363
Leu Ala Ile Ser Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys
      65      70      75
gtg ggg gcc ctc aag gag ctc cgc tgc ctc ctg ggc ctg tat ttt ggg 411
Val Gly Ala Leu Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly
      80      85      90
atg ctg ctg ctc ctg ttt gcc aca cag atc acc ctg gga atc ctc atc 459
Met Leu Leu Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile
      95      100      105
tcc act cag cgg gcc agc tgg agc gaa gct tgc ggg acg tcg 501
Ser Thr Gln Arg Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser
      110      115      120
tagagaaaac catccaaaag tacggcacca accccgagga gaccgcggcc gaggagagct 561
gggactatgt gcagttccag ctgcgtgct gcggctggca ctaccgcag gactggttcc 621
aagtcctcat cctgagaggt aacgggtcgg aggcgcaccg cgtgccctgc tctgtctaca 681
acttgctcggc gaccaacgac tccacaatcc tagataaggt gatcttgccc cagctcagca 741
ggcttggaaca cctggcgagg tccagacaca gtgcagacat ctgcgtgtc cctgcagaga 801
gccacatcta ccgcgagggc tgccgcgcagg gcctccagaa gtgggtgcac aacaacctta 861
tttccatagt gggcatttgc ctgggcgtcg gcctactcga gctcgggttc atgacgtct 921
cgatattcct gtgcagaaac ctggaccacg tctacaaccg gctcgtcga taccgttagg 981
ccccgccttc cccaaagtcc cgccccgccc ccgtcacgtg cgctgggcac ttccctgctg 1041
cctgtaaata tttgtttaat ccccagttcg cctggagccc tctctcttca cattccccctg 1101
gggaccacag tggctgcgtg ccctgctgc tgtcacctct cccacgggac ctggggcttt 1161
cgctccacagc ttctgttccc catctgtcgg cctaccacca cccacaagat tatttttcac 1221
ccaaacctca aataaatccc ctgcgttttt ggtaaaaaaa aaaaaaaaaa aaaaaaaaaa 1281
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa amcaaaaaaa aaaaaaaaaa 1340

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<210> 44  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

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<400> 44
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1      5      10      15
Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
      20      25      30
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
      35      40      45
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
      50      55      60

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Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu  
 65 70 75 80  
 Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu  
 85 90 95  
 Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg  
 100 105 110  
 Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser  
 115 120

<210> 45  
 <211> 1999  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..117

<220>  
 <221> CDS  
 <222> 118..1632

<220>  
 <221> 3'UTR  
 <222> 1633..1999

<220>  
 <221> polyA\_signal  
 <222> 1937..1942

<220>  
 <221> polyA\_site  
 <222> 1956..1999

<400> 45  
 aggtccgcct gggccagacg cgcgagcgca agcagcgggt tagtggtcgc gcgcccgacc 60  
 tccgcagtcc cagccgagcc gcgacccttc cggccgtccc caccacacct cgccgcc 117  
 atg cgc ctc cgc cgc cta gcg ctg ttc ccg ggt gtg gcg ctg ctt ctt 165  
 Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu  
 -20 -15 -10  
 gcc gcg gcc cgc ctc gcc gct gcc tcc gac gtg cta gaa ctc acg gac 213  
 Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp  
 -5 1 5  
 gac aac ttc gag agt cgc atc tcc gac acg ggc tct gcg ggc ctc atg 261  
 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met  
 10 15 20  
 ctc gtc gag ttc ttc gct ccc tgg tgt gga cac tgc aag aga ctt gca 309  
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala  
 25 30 35 40  
 cct gag tat gaa gct gca gct acc aga tta aaa gga ata gtc cca tta 357  
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu  
 45 50 55  
 gca aag gtt gat tgc act gcc aac act aac acc tgt aat aaa tat gga 405  
 Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly  
 60 65 70



gtc agt gga tat cca acc ctg aag ata ttt aga gat ggt gaa gaa gca	453
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala	
75 80 85	
ggg gct tat gat gga cct agg act gct gat gga att gtc agc cac ttg	501
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu	
90 95 100	
aag aag cag gca gga cca gct tca gtg cct ctg agg act gag gaa gaa	549
Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu	
105 110 115 120	
ttt aag aaa ttc att agt gat aaa gat gcc tct ata gta ggt ttt ttc	597
Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe	
125 130 135	
gat gat tca ttc agt gag gct cac tcc gag ttc cta aaa gca gcc agc	645
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser	
140 145 150	
aac ttg agg gat aac tac cga ttt gca cat acg aat gtt gag tct ctg	693
Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu	
155 160 165	
gtg aac gag tat gat gat aat gga gag ggt atc atc tta ttt cgt cct	741
Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro	
170 175 180	
tca cat ctg act aac aag ttt gag gac aag act gtg gca tat aca gag	789
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu	
185 190 195 200	
caa aaa atg acc agt ggc aaa att aaa aag ttt atc cag gaa aac att	837
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile	
205 210 215	
ttt ggt atc tgc cct cac atg aca gaa gac aat aaa gat ttg ata cag	885
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln	
220 225 230	
ggc aag gac tta ctt att gct tac tat gat gtg gac tat gaa aag aac	933
Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn	
235 240 245	
gct aaa ggt tcc aac tac agg aga aac agg gta atg atg gtg gca aag	981
Ala Lys Gly Ser Asn Tyr Arg Arg Asn Arg Val Met Met Val Ala Lys	
250 255 260	
aaa ttc ctg gat gct ggg cac aaa ctg aac ttt gct gta gct agc cgc	1029
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg	
265 270 275 280	
aaa acc ttt agc cat gaa ctt tct gat ttt ggc ttg gag agc act gct	1077
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala	
285 290 295	
gga gag att cct gtt gtt gct atc aga act gct aaa gga gag aag ttt	1125
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe	
300 305 310	
gtc atg cag gag gag ttc tcg cgt gat ggg aag gct ctg gag agg ttc	1173
Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe	
315 320 325	
ctg cag gat tac ttt gat ggc aat ctg aag aga tac ctg aag tct gaa	1221
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu	
330 335 340	
cct atc cca gag agc aat gat ggg cct gtg aag gta gtg gta gca gag	1269
Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu	
345 350 355 360	
aat ttt gat gaa ata gtg aat aat gaa aat aaa gat gtg ctg att gaa	1317

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Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
      365      370      375
ttt tat gcc cct tgg tgt ggt cat tgt aag aac ctg gag ccc aag tat 1365
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
      380      385      390
aaa gaa ctt ggc gag aag ctc agc aaa gac cca aat atc gtc ata gcc 1413
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
      395      400      405
aag atg gat gcc aca gcc aat gat gtg cct tct cca tat gaa gtc aga 1461
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
      410      415      420
ggt ttt cct acc ata tac ttc tct cca gcc aac aag aag cta aat cca 1509
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
      425      430      435      440
aag aaa tat gaa ggt ggc cgt gaa tta agt gat ttt att agc tat cta 1557
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
      445      450      455
caa aga gaa gct aca atc ccc cct gta att caa gaa gaa aaa ccc aag 1605
Gln Arg Glu Ala Thr Ile Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
      460      465      470
aag aag aag aag gca cag gag gat ctc taaagcagta gccaaacacc 1652
Lys Lys Lys Lys Ala Gln Glu Asp Leu
      475      480
actttgtaaa aggactcttc catcagagat gggaaaacca ttggggagga ctaggaccca 1712
tatgggaatt attacctctc agggccgaga ggacagaatg gatataatct gaatcctgtt 1772
aaattttctc taaactgttt cttagctgca ctgtttatgg aaataccagg accagtttat 1832
gtttgtgggt ttgggaaaaa ttatttgtgt tgggggaaat gttgtggggg tggggttgag 1892
ttgggggtat tttctaattt tttttgtaca tttggaacag tgacaataaa tgagaccctt 1952
tttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaawaaaa aaaaaaaa 1999

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<210> 46  
 <211> 505  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..24

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<400> 46
Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
      -20      -15      -10
Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
      -5      1      5
Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
      10      15      20
Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
      25      30      35      40
Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
      45      50      55
Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
      60      65      70
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
      75      80      85
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu

```

90	95	100
Lys Lys Gln Ala Gly	Pro Ala Ser Val	Pro Leu Arg Thr Glu Glu Glu
105	110	115
Phe Lys Lys Phe Ile	Ser Asp Lys Asp	Ala Ser Ile Val Gly Phe Phe
125	130	135
Asp Asp Ser Phe Ser	Glu Ala His Ser	Glu Phe Leu Lys Ala Ala Ser
140	145	150
Asn Leu Arg Asp Asn	Tyr Arg Phe Ala	His Thr Asn Val Glu Ser Leu
155	160	165
Val Asn Glu Tyr Asp	Asp Asn Gly Glu	Gly Ile Ile Leu Phe Arg Pro
170	175	180
Ser His Leu Thr Asn	Lys Phe Glu Asp	Lys Thr Val Ala Tyr Thr Glu
185	190	195
Gln Lys Met Thr Ser	Gly Lys Ile Lys	Lys Phe Ile Gln Glu Asn Ile
205	210	215
Phe Gly Ile Cys Pro	His Met Thr Glu	Asp Asn Lys Asp Leu Ile Gln
220	225	230
Gly Lys Asp Leu Leu	Ile Ala Tyr Tyr	Asp Val Asp Tyr Glu Lys Asn
235	240	245
Ala Lys Gly Ser Asn	Tyr Arg Asn Arg	Val Met Met Val Ala Lys
250	255	260
Lys Phe Leu Asp Ala	Gly His Lys Leu	Asn Phe Ala Val Ala Ser Arg
265	270	275
Lys Thr Phe Ser His	Glu Leu Ser Asp	Phe Gly Leu Glu Ser Thr Ala
285	290	295
Gly Glu Ile Pro Val	Val Ala Ile Arg	Thr Ala Lys Gly Glu Lys Phe
300	305	310
Val Met Gln Glu Glu	Phe Ser Arg Asp	Gly Lys Ala Leu Glu Arg Phe
315	320	325
Leu Gln Asp Tyr Phe	Asp Gly Asn Leu	Lys Arg Tyr Leu Lys Ser Glu
330	335	340
Pro Ile Pro Glu Ser	Asn Asp Gly Pro	Val Lys Val Val Val Ala Glu
345	350	355
Asn Phe Asp Glu Ile	Val Asn Asn Glu	Asn Lys Asp Val Leu Ile Glu
365	370	375
Phe Tyr Ala Pro Trp	Cys Gly His Cys	Lys Asn Leu Glu Pro Lys Tyr
380	385	390
Lys Glu Leu Gly Glu	Lys Leu Ser Lys	Asp Pro Asn Ile Val Ile Ala
395	400	405
Lys Met Asp Ala Thr	Ala Asn Asp Val	Pro Ser Pro Tyr Glu Val Arg
410	415	420
Gly Phe Pro Thr Ile	Tyr Phe Ser Pro	Ala Asn Lys Lys Leu Asn Pro
425	430	435
Lys Lys Tyr Glu Gly	Gly Arg Glu Leu	Ser Asp Phe Ile Ser Tyr Leu
445	450	455
Gln Arg Glu Ala Thr	Ile Pro Pro Val	Ile Gln Glu Glu Lys Pro Lys
460	465	470
Lys Lys Lys Lys Ala	Gln Glu Asp Leu	
475	480	

&lt;210&gt; 47

&lt;211&gt; 836

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
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 <222> 1..153

<220>  
 <221> CDS  
 <222> 154..546

<220>  
 <221> 3'UTR  
 <222> 547..836

<220>  
 <221> polyA\_site  
 <222> 722..836

<400> 47  
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 tcgcccgtgc cgggttcattg ctcacaagca gacagctcct ccgcctctga tgcagaattt 120  
 gatgctgtgg ttggatattt agaggacatt atc atg gat gac gag ttc cag tta 174  
 Met Asp Asp Glu Phe Gln Leu  
 1 5  
 tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222  
 Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr  
 10 15 20  
 gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270  
 Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser  
 25 30 35  
 ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318  
 Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu  
 40 45 50 55  
 ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366  
 Phe Asn Met Ala Ala Phe Thr Thr Thr Leu Gln His His Lys Asp Glu  
 60 65 70  
 gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414  
 Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu  
 75 80 85  
 gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462  
 Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg  
 90 95 100  
 gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510  
 Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser  
 105 110 115  
 tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556  
 Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His  
 120 125 130  
 ctccagccaa tgaatgggat cattctggat gtcaccagcc caataggctc agctcatgat 616  
 gacagaacac atcttggaat gactgactct gttatgtaac tcttcattta tgtaagtat 676  
 taataggtca aaacccaaat gacctaacc tcttgacat atttcaaaaa aaaaaaaaaa 736  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 796  
 aaaaaaaaaa aaaaaaaaaa aaaagaaaaa aaaaaaaaaa 836

<210> 48  
 <211> 131  
 <212> PRT

<213> Homo sapiens

<400> 48

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Met Asp Asp Glu Phe Gln Leu Leu Gln Arg Asn Phe Met Asp Lys Tyr
1           5           10           15
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro
           20           25           30
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
           35           40           45
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
           50           55           60
Leu Gln His His Lys Asp Glu Val Ala Gly Asp Ile Phe Asp Met Leu
65           70           75           80
Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys Glu Met Phe Leu Asp Tyr
           85           90           95
Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp Leu Ser Ser Gly Leu Val
           100          105          110
Val Thr Ser Leu Cys Lys Ser Ser Leu Pro Ala Ser Gln Asn Asn
           115          120          125
Leu Arg His
           130

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<210> 49

<211> 862

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..195

<220>

<221> CDS

<222> 196..708

<220>

<221> 3'UTR

<222> 709..862

<220>

<221> polyA\_site

<222> 847..862

<400> 49

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cggaggcagc tggggaggtc cgagcgatgt gaccaggccg ccatcgctcg tctcttcctc 120
tctcctgccg cctcctgtct cgtaaataac ttttttactc taaagaaaga aagacaaaag 180
tagtcgtccg ccccc atg cat ccc ttc tac acc cgg gcc gcc acc atg ata 231
           Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile
           1           5           10
ggc gag atc gcc gcc gcc gtg tcc ttc atc tcc aag ttt ctc cgc acc 279
Gly Glu Ile Ala Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr
           15           20           25
aag ggg ctc acg agc gag cga cag ctg cag acc ttc agc cag agc ctg 327
Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu

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```

      30              35              40
cag gag ctg ctg gca gaa cat tat aaa cat cac tgg ttc cca gaa aag 375
Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys
45              50              55              60
cca tgc aag gga tgc ggt tac cgt tgt att cgc atc aac cat aaa atg 423
Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met
      65              70              75
gat cct ctg att gga cag gca gca cag cgg att gga ctg agc agt cag 471
Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln
      80              85              90
gag ctg ttc agg ctt ctc cca agt gaa ctc aca ctc tgg gtt gac ccc 519
Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro
      95              100              105
tat gaa gtg tcc tac aga att gga gag gat ggc tcc atc tgt gtg ctg 567
Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu
      110              115              120
tat gaa gcc tca cca gca gga ggt agc act caa aac agc acc aac gtg 615
Tyr Glu Ala Ser Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val
      125              130              135              140
caa atg gta gac agc cga atc agc tgt aag gag gaa ctt ctc ttg ggc 663
Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly
      145              150              155
aga acg agc cct tcc aaa aac tac aat atg atg act gta tca agt 708
Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser
      160              165              170
taagatatag tctgtggatg gatcatctga tgatgatgga taaatttgat ttttgctttg 768
gggtgggctcc tcttggggat ggattatgga atttaaacca tgtcacagct gtgaagatct 828
ggcacaagat agaatggcaa aaaaaaaaaa aaaa 862

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&lt;210&gt; 50

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

```

Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile Gly Glu Ile Ala
1              5              10              15
Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr Lys Gly Leu Thr
      20              25              30
Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu Gln Glu Leu Leu
      35              40              45
Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys Pro Cys Lys Gly
      50              55              60
Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Leu Ile
      65              70              75              80
Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln Glu Leu Phe Arg
      85              90              95
Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser
      100              105              110
Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Ala Ser
      115              120              125
Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val Gln Met Val Asp
      130              135              140
Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly Arg Thr Ser Pro
      145              150              155              160

```

<400>	51																			
gaggaaagag	tc	at	ca	gag	gat	ca	gc	cag	tcc	ag	gga	g	cc	gt	gc	ccc	gct	tct	cta	60
a	at	g	cca	ctc	ccc	ctc	cca	tca	gc	g	ttc	gtg	ctg	tca	gcc	ttg	cag	cct		109
	Met	Pro	Leu	Pro	Leu	Pro	Ser	Ala	Phe	Val	Leu	Ser	Ala	Leu	Gln	Pro				
	-20				-15				-10											
tct	cct	act	cat	tcc	agc	tcc	aat	acc	cag	cgg	ctg	cca	gac	cga	gtg					157
Ser	Pro	Thr	His	Ser	Ser	Ser	Asn	Thr	Gln	Arg	Leu	Pro	Asp	Arg	Val					
	-5				1				5					10						
acc	ggc	ggc	ttc	tca	gtg	aat	gga	cag	ctc	att	ggc	aac	aag	gcc	agg					205
Thr	Gly	Gly	Phe	Ser	Val	Asn	Gly	Gln	Leu	Ile	Gly	Asn	Lys	Ala	Arg					
			15					20					25							
agc	cct	ggg	cag	cat	gac	ggc	acg	tac	ttc	ggg	cgg	ctg	gga	atc	gca					253
Ser	Pro	Gly	Gln	His	Asp	Gly	Thr	Tyr	Phe	Gly	Arg	Leu	Gly	Ile	Ala					
		30					35				40									
aac	cct	gcc	acg	gac	ttt	cag	ttg	gaa	gtg	act	cct	cag	aac	att	acg					301
Asn	Pro	Ala	Thr	Asp	Phe	Gln	Leu	Glu	Val	Thr	Pro	Gln	Asn	Ile	Thr					
	45					50				55										
ctg	aac	ccc	ggc	ttt	ggt	ggg	cct	gtg	tgt	tcc	tgg	agg	gac	caa	gct					349
Leu	Asn	Pro	Gly	Phe	Gly	Gly	Pro	Val	Phe	Ser	Trp	Arg	Asp	Gln	Ala					
60					65				70					75						
gtg	ctg	cgg	cag	gac	ggg	gtg	gtg	gtg	acc	atc	aac	aag	aag	agg	aac					397
Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Lys	Arg	Asn					
				80					85					90						
ctg	gtg	gtg	tct	gtg	gac	gac	ggt	ggc	acc	ttt	gag	gtt	gtt	ttg	cac					445
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Val	Leu	His					
			95				100						105							
cga	gtg	tgg	aag	ggg	agc	tcg	gtc	cac	cag	qac	ttc	ctg	ggc	ttc	tat					493

```

Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
      110      115      120
gtg ctg gac agt cat cgg atg tca gcc cgg acg cac ggg ctg ctg ggg 541
Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
      125      130      135
caa ttt ttc cac ccc atc ggt ttt gaa gtg tct gac atc cac cca ggc 589
Gln Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly
      140      145      150      155
tct gac ccc aca aag cca gat gcc acg atg gtg gtg agg aac cgc cgg 637
Ser Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg
      160      165      170
ctc acg gtc acc agg ggt ttg caa aaa gac tac agc aag gac ccg tgg 685
Leu Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp
      175      180      185
cat ggg gcc gag gtg tcc tgc tgg ttc att cac aac aat ggg gct gga 733
His Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly
      190      195      200
ctc atc gat ggt gcc tac act gat tat atc gtc ccc gac atc ttc 778
Leu Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe
      205      210      215
tgagccctct ggccagcacg cctgtcctcc cccggggcca aggcagagga ggaggacgac 838
atcctgacct gctgctgagg ctgtacctcc ttgactaagc tggttccttg tgtcaaagca 898
cctcatgcct tccattaaag agaggccgtg tccaaaaaaa aaaaaaaaaa 947

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&lt;210&gt; 52

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..21

&lt;400&gt; 52

```

Met Pro Leu Pro Leu Pro Ser Ala Phe Val Leu Ser Ala Leu Gln Pro
      -20      -15      -10
Ser Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val
      -5      1      5      10
Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
      15      20      25
Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
      30      35      40
Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
      45      50      55
Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala
      60      65      70      75
Val Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn
      80      85      90
Leu Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His
      95      100      105
Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
      110      115      120
Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
      125      130      135
Gln Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly

```



```

140          145          150          155
Ser Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg
          160          165          170
Leu Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp
          175          180          185
His Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly
          190          195          200
Leu Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe
          205          210          215

```

```

<210> 53
<211> 23
<212> PRT
<213> Homo sapiens

```

```

<400> 53
Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val Val Gly
1          5          10          15
Leu Val Ala Leu Gly Ile Trp
          20

```

```

<210> 54
<211> 90
<212> PRT
<213> Homo sapiens

```

```

<400> 54
Gln Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg
1          5          10          15
Asn Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val
          20          25          30
Gly Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly
          35          40          45
Ser Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly
          50          55          60
Asn Met Asn Cys Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe
65          70          75          80
Cys Glu Asn Lys His Tyr Leu Met Cys Glu
          85          90

```

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<210> 55
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 55
Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met
1          5          10          15
Asn Ala Thr Leu
          20

```

```

<210> 56
<211> 50
<212> PRT
<213> Homo sapiens

```

&lt;400&gt; 56

Met Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln  
 1 5 10 15  
 Pro Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro  
 20 25 30  
 His Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser  
 35 40 45  
 Phe Ile  
 50

&lt;210&gt; 57

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

His Glu Leu Gly His Asn Leu Gly Met Gln His Asp  
 1 5 10

&lt;210&gt; 58

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

Glu Glu Gly Glu Glu Cys Asp Cys Gly  
 1 5

&lt;210&gt; 59

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro Cys  
 1 5 10 15  
 Thr

&lt;210&gt; 60

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

Leu Asn Ser Ser Glu Gly Gly Ala Arg  
 1 5

&lt;210&gt; 61

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

Cys Ser Ser Gly Leu Gln Ala Val Ala Ser Ile Ala Gly Trp Ser Pro

1                    5                    10                    15  
 Cys Pro Trp Leu Thr  
                   20

<210> 62  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Ala Pro Gln Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg  
 1                    5                    10                    15  
 Thr Ala Ile Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro  
                   20                    25                    30  
 Asp Glu Leu Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn  
                   35                    40                    45  
 Leu Arg Pro Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln  
                   50                    55                    60  
 Pro Gly Ala Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp  
 65                    70                    75                    80  
 Ile Pro Glu Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser  
                   85                    90                    95  
 Gly Leu Gln Ala Val Ala Ser Ile Ala Gly Trp Ser Pro Cys Pro Trp  
                   100                    105                    110  
 Leu Thr Glu Gly Thr Leu Glu Ile Leu  
                   115                    120

<210> 63  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 63  
 Met Pro Phe Ser His Leu Ser Thr Tyr Ser Leu Val Trp Val Met Ala  
 1                    5                    10                    15  
 Ala Val Val Leu Cys Thr Ala  
                   20

<210> 64  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Val Pro Leu Leu Leu Ser Ile Val Ser Leu Val Ile Leu Leu Val Leu  
 1                    5                    10                    15  
 Ile Ser Ile Leu Leu Tyr Trp  
                   20

<210> 65  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<400> 65

Thr Ala Ser Leu Lys Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile  
 1                   5                   10                   15  
 Val Thr Trp Gln Lys Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr  
                  20                   25                   30  
 Phe Ser Glu Asn His Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys  
          35                   40                   45  
 Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp  
      50                   55                   60  
 Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr Met Cys Leu Phe  
 65                   70                   75

<210> 66  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala Pro  
 1                   5                   10                   15  
 Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr Val  
                  20                   25                   30  
 Thr Leu Ser His Pro Asn Gly Thr Ser Val Thr Ser Ile Leu His  
      35                   40                   45  
 Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln Val  
      50                   55                   60

<210> 67  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 67  
 Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro Ile Leu  
 1                   5                   10                   15  
 Val Trp Leu Phe Thr  
                  20

<210> 68  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Val Leu Leu Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala  
 1                   5                   10                   15  
 Ser Tyr Leu Val Trp  
                  20

<210> 69  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu

1                    5                    10                    15  
 Phe Phe Thr Val His  
                   20

<210> 70  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Gly Leu Ala Leu Leu His Leu Leu Leu Leu Tyr Gly Leu Val Val Ser  
 1                    5                    10                    15  
 Thr Ala Leu Ile Trp  
                   20

<210> 71  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 71  
 Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val Thr  
 1                    5                    10                    15  
 Ser Ala Leu Thr Tyr  
                   20

<210> 72  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg  
 1                    5                    10

<210> 73  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu Phe  
 1                    5                    10                    15  
 Phe Thr Val His Asn  
                   20

<210> 74  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
 Leu Ala Leu Leu His Leu Leu Leu Leu Tyr Gly Leu Val Val Ser Thr  
 1                    5                    10                    15  
 Ala Leu Ile Trp His

20

<210> 75  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 75  
 Leu Leu His Asn His Leu Thr Val Arg Val Ile Glu Ala Arg Asp Leu  
 1 5 10 15  
 Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln Asp Met Ala His Ser  
 20 25 30  
 Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp Gln Lys Asn Ser Lys  
 35 40 45  
 Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro Val Phe Glu Glu Arg  
 50 55 60  
 Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln Arg Arg Thr Leu Leu  
 65 70 75 80  
 Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg His Cys Val Ile Gly  
 85 90 95  
 Lys Val Ser

<210> 76  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
 Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln Thr  
 1 5 10 15  
 Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val His  
 20 25 30  
 Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly Thr  
 35 40 45  
 Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln Glu  
 50 55 60  
 Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn Met  
 65 70 75 80  
 Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly  
 85 90

<210> 77  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
 Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu  
 1 5 10 15  
 Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr Asp Arg  
 20 25 30  
 Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu Gly Asn  
 35 40 45  
 Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Leu Ala Gly Gly  
 50 55 60

<210> 78  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu  
 1 5 10 15  
 Thr Glu Ala Ala Leu Gly Asp Ala  
 20

<210> 79  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<400> 79  
 Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg  
 1 5 10 15  
 Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly  
 20 25 30  
 Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp  
 35 40 45  
 Asp Leu Ala  
 50

<210> 80  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser Ala Phe Ser  
 1 5 10 15  
 Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser Gln Thr Ser  
 20 25 30  
 Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys Met Ala Arg  
 35 40 45  
 Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu Asn Asn Met  
 50 55 60  
 Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser Glu Ala Pro  
 65 70 75 80  
 Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu Gln Glu Glu  
 85 90 95  
 Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His  
 100 105 110  
 Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln Leu Lys Pro  
 115 120 125  
 Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Gln Glu Leu  
 130 135 140  
 Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala Gln Leu Leu  
 145 150 155 160  
 Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu Gln Ser Arg  
 165 170 175  
 Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His Pro Tyr Ala

```

      180      185      190
Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu Leu His Arg
      195      200      205
Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu Ser Arg Cys
      210      215      220
Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys Ala Leu His
225      230      235      240
Ala Arg Ile Gln Gln Asn Leu Asp
      245

```

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<210> 81
<211> 107
<212> PRT
<213> Homo sapiens

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```

<400> 81
Phe Lys Thr Leu Gln Arg Asn Gly Leu Met Leu His Thr Gly Lys Ser
1      5      10      15
Ala Asp Tyr Val Asn Leu Ala Leu Lys Asn Gly Ala Val Ser Leu Val
      20      25      30
Ile Asn Leu Gly Ser Gly Ala Phe Glu Ala Leu Val Glu Pro Val Asn
      35      40      45
Gly Lys Phe Asn Asp Asn Ala Trp His Asp Val Lys Val Thr Arg Asn
      50      55      60
Leu Arg Gln Val Thr Ile Ser Val Asp Gly Ile Leu Thr Thr Thr Gly
65      70      75      80
Tyr Thr Gln Glu Asp Tyr Thr Met Leu Gly Ser Asp Asp Phe Phe Tyr
      85      90      95
Val Gly Gly Ser Pro Ser Thr Ala Asp Leu Pro
      100      105

```

```

<210> 82
<211> 35
<212> PRT
<213> Homo sapiens

```

```

<400> 82
Val Met Ser Phe Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val
1      5      10      15
Gly Arg Ser Lys Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu
      20      25      30
Gln Leu Val
      35

```

```

<210> 83
<211> 58
<212> PRT
<213> Homo sapiens

```

```

<400> 83
Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val Pro Cys
1      5      10      15
Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val Phe Tyr
      20      25      30
Leu Gln Met Asn Glu Lys Glu Thr Cys Ala His Leu Gln Cys Phe Asp

```



35 40 45  
 Ala Val Phe Tyr Leu Gln Met Asn Glu Lys  
 50 55

<210> 84  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser  
 1 5 10 15  
 Trp Gly

<210> 85  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 85  
 Ser Leu Gln Asp Ser Ser Asp Phe His Phe  
 1 5 10

<210> 86  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly  
 1 5 10 15  
 Pro Arg Thr His Met Gln Ala  
 20

<210> 87  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 87  
 Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu Ser Leu Leu  
 1 5 10 15  
 Leu Phe Leu Leu Leu  
 20

<210> 88  
 <211> 424  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile  
 1 5 10 15  
 Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu Ala  
 20 25 30

```

Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp Arg
   35           40           45
Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro Ser
   50           55           60
Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser Pro
  65           70           75           80
Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr Gly
           85           90           95
Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val Thr
           100           105           110
Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met Asp
           115           120           125
Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His Leu
  130           135           140
Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met Ser
  145           150           155           160
Pro Val Thr Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser His
           165           170           175
Gly Phe Ser His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu Leu
           180           185           190
Ile Val Ser Gly Ser Leu Glu Asp Pro Arg Pro Ser Pro Thr Arg Ser
           195           200           205
Val Ser Thr Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr Gly
  210           215           220
Ser Val Pro His Ser Gly Leu Arg Arg His Trp Glu Val Leu Ile Gly
  225           230           235           240
Val Leu Val Val Ser Ile Leu Leu Leu Ser Leu Leu Leu Phe Leu Leu
           245           250           255
Leu Gln His Trp Arg Gln Gly Lys His Arg Thr Leu Ala Gln Arg Gln
           260           265           270
Ala Asp Phe Gln Arg Pro Pro Gly Ala Ala Glu Pro Glu Pro Lys Asp
           275           280           285
Gly Gly Leu Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly Glu
  290           295           300
Asn Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val Glu
  305           310           315           320
Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
           325           330           335
Ala Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
           340           345           350
Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu
           355           360           365
Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln
           370           375           380
Asp Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys Ala
  385           390           395           400
Thr Glu Pro Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro Ser
           405           410           415
Val Tyr Ala Thr Leu Ala Ile His
           420

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&lt;210&gt; 89

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile  
 1 5 10 15  
 Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu Ala  
 20 25 30  
 Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp Arg  
 35 40 45  
 Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro Ser  
 50 55 60  
 Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser Pro  
 65 70 75 80  
 Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr Gly  
 85 90 95  
 Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val Thr  
 100 105 110  
 Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met Asp  
 115 120 125  
 Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His Leu  
 130 135 140  
 Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met Ser  
 145 150 155 160  
 Pro Val Thr Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser His  
 165 170 175  
 Gly Phe Ser His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu Leu  
 180 185 190  
 Ile Val Ser Gly Ser Leu Glu Asp Pro Arg Pro Ser Pro Thr Arg Ser  
 195 200 205  
 Val Ser Thr Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr Gly  
 210 215 220  
 Ser Val Pro His Ser Gly Leu Arg Arg His Trp Glu  
 225 230 235

&lt;210&gt; 90

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

Gln His Trp Arg Gln Gly Lys His Arg Thr Leu Ala Gln Arg Gln Ala  
 1 5 10 15  
 Asp Phe Gln Arg Pro Pro Gly Ala Ala Glu Pro Glu Pro Lys Asp Gly  
 20 25 30  
 Gly Leu Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly Glu Asn  
 35 40 45  
 Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val Glu Met  
 50 55 60  
 Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala  
 65 70 75 80  
 Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser  
 85 90 95  
 Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu  
 100 105 110  
 Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp  
 115 120 125

Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys Ala Thr  
 130 135 140  
 Glu Pro Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro Ser Val  
 145 150 155 160  
 Tyr Ala Thr Leu Ala Ile His  
 165

<210> 91  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
 Met Arg Thr Tyr Trp Leu His Ser Val Trp Val Leu Gly Phe Phe Leu  
 1 5 10 15  
 Ser Leu Phe Ser Leu Gln  
 20

<210> 92  
 <211> 361  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
 Gly Leu Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile  
 1 5 10 15  
 Thr Val Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp  
 20 25 30  
 Lys Asn Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala  
 35 40 45  
 Gly His Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg  
 50 55 60  
 His Ser Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp  
 65 70 75 80  
 Glu Gly Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr  
 85 90 95  
 Ser Gln Val Tyr Leu Ile Val Gln Val Pro Pro Lys Ile Ser Asn Ile  
 100 105 110  
 Ser Ser Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys  
 115 120 125  
 Met Ala Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr  
 130 135 140  
 Pro Thr Gly Arg Glu Phe Glu Gly Glu Glu Glu Tyr Leu Glu Ile Leu  
 145 150 155 160  
 Gly Ile Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn  
 165 170 175  
 Glu Val Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr  
 180 185 190  
 Pro Pro Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg  
 195 200 205  
 Gln Ala Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe  
 210 215 220  
 Glu Trp Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu  
 225 230 235 240  
 Ile Lys Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr

				245					250					255			
Glu	Glu	His	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ala	Asn	Lys	Leu	Gly		
			260					265					270				
Val	Thr	Asn	Ala	Ser	Leu	Val	Leu	Phe	Lys	Arg	Val	Leu	Pro	Thr	Ile		
		275					280					285					
Pro	His	Pro	Ile	Gln	Glu	Ile	Gly	Thr	Thr	Val	His	Phe	Lys	Gln	Lys		
	290					295					300						
Gly	Ile	Phe	Leu	Ser	Glu	Ser	Gln	Arg	Gly	Glu	Thr	Thr	Lys	Ile	Thr		
305					310				315					320			
Leu	Asn	Cys	Gly	Asn	Leu	Phe	Leu	Arg	Asn	Leu	His	Pro	Thr	Ser	Asp		
			325					330					335				
Gln	Glu	Pro	Gln	Arg	Leu	Trp	Thr	Leu	Cys	Cys	Leu	Leu	Pro	Arg	Lys		
			340				345						350				
Gly	Gln	His	Arg	Ile	Tyr	Gly	Gln	Cys									
		355					360										

&lt;210&gt; 93

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

Gly	Leu	Pro	Val	Arg	Ser	Val	Asp	Phe	Asn	Arg	Gly	Thr	Asp	Asn	Ile		
1			5					10					15				
Thr	Val	Arg	Gln	Gly	Asp	Thr	Ala	Ile	Leu	Arg	Cys	Val	Val	Glu	Asp		
			20				25					30					
Lys	Asn	Ser	Lys	Val	Ala	Trp	Leu	Asn	Arg	Ser	Gly	Ile	Ile	Phe	Ala		
		35				40					45						
Gly	His	Asp	Lys	Trp	Ser	Leu	Asp	Pro	Arg	Val	Glu	Leu	Glu	Lys	Arg		
	50				55			60									
His	Ser	Leu	Glu	Tyr	Ser	Leu	Arg	Ile	Gln	Lys	Val	Asp	Val	Tyr	Asp		
65				70				75						80			
Glu	Gly	Ser	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Gln	His	Glu	Pro	Lys	Thr		
			85				90						95				
Ser	Gln	Val	Tyr	Leu	Ile	Val	Gln	Val	Pro	Pro	Lys	Ile	Ser	Asn	Ile		
		100				105						110					
Ser	Ser	Asp	Val	Thr	Val	Asn	Glu	Gly	Ser	Asn	Val	Thr	Leu	Val	Cys		
		115				120					125						
Met	Ala	Asn	Gly	Arg	Pro	Glu	Pro	Val	Ile	Thr	Trp	Arg	His	Leu	Thr		
	130				135			140									
Pro	Thr	Gly	Arg	Glu	Phe	Glu	Gly	Glu	Glu	Glu	Tyr	Leu	Glu	Ile	Leu		
145				150				155						160			
Gly	Ile	Thr	Arg	Glu	Gln	Ser	Gly	Lys	Tyr	Glu	Cys	Lys	Ala	Ala	Asn		
			165				170						175				
Glu	Val	Ser	Ser	Ala	Asp	Val	Lys	Gln	Val	Lys	Val	Thr	Val	Asn	Tyr		
			180				185					190					
Pro	Pro	Thr	Ile	Thr	Glu	Ser	Lys	Ser	Asn	Glu	Ala	Thr	Thr	Gly	Arg		
		195				200					205						
Gln	Ala	Ser	Leu	Lys	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ala	Pro	Asp	Phe		
	210				215					220							
Glu	Trp	Tyr	Arg	Asp	Asp	Thr	Arg	Ile	Asn	Ser	Ala	Asn	Gly	Leu	Glu		
225				230				235						240			
Ile	Lys	Ser	Thr	Glu	Gly	Gln	Ser	Ser	Leu	Thr	Val	Thr	Asn	Val	Thr		
			245				250						255				
Glu	Glu	His	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ala	Asn	Lys	Leu	Gly		

260 265 270  
 Val Thr Asn Ala Ser Leu Val Leu Phe  
 275 280

<210> 94  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
 Lys Arg Val Leu Pro Thr Ile Pro His Pro Ile Gln Glu Ile Gly Thr  
 1 5 10 15  
 Thr Val His Phe Lys Gln Lys Gly Ile Phe Leu Ser Glu Ser Gln Arg  
 20 25 30  
 Gly Glu Thr Thr Lys Ile Thr Leu Asn Cys Gly Asn Leu Phe Leu Arg  
 35 40 45  
 Asn Leu His Pro Thr Ser Asp Gln Glu Pro Gln Arg Leu Trp Thr Leu  
 50 55 60  
 Cys Cys Leu Leu Pro Arg Lys Gly Gln His Arg Ile Tyr Gly Gln Cys  
 65 70 75 80

<210> 95  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
 Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp  
 1 5 10 15  
 Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu Ala Ala Leu  
 20 25 30  
 Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp  
 35 40 45  
 Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile Leu Val Glu  
 50 55 60  
 Val Trp Ile Leu Pro Ser Cys Ala  
 65 70

<210> 96  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu  
 1 5 10 15  
 Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val  
 20 25 30  
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly  
 35 40 45  
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe  
 50 55 60  
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg  
 65 70 75 80  
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro

```

      85              90              95
Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
      100              105              110
Ser Leu His Thr Pro Arg Ser Arg Pro Ser Pro Gly Pro Ser Thr
      115              120              125
Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
      130              135              140

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<210> 97
<211> 105
<212> PRT
<213> Homo sapiens

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```

<400> 97
Ala His Ser Gly Leu Trp Pro Thr Gly His Gly Asp Ile Ile Ser Gly
1      5      10      15
His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe Ala Ala Gly Lys Asp
      20      25      30
Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg Ile Pro Ala Glu Glu
      35      40      45
Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro Ser Pro Trp Trp Trp
      50      55      60
Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr Ser Leu His Thr Pro
65      70      75      80
Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr Trp Ala Gly Ser Gln
      85      90      95
Leu Ser Ser Cys Ser Val Gln Val Pro
      100      105

```

```

<210> 98
<211> 37
<212> PRT
<213> Homo sapiens

```

```

<400> 98
Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
1      5      10      15
Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
      20      25      30
Gly Pro Thr His Ser
      35

```

```

<210> 99
<211> 21
<212> PRT
<213> Homo sapiens

```

```

<400> 99
Gly Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala
1      5      10      15
Phe Ala Ala Gly Lys
      20

```

```

<210> 100
<211> 50

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<212> PRT  
 <213> Homo sapiens

<400> 100  
 Ser Cys Pro Cys Pro Gln Pro Ser Pro Trp Trp Trp Pro Trp Arg Cys  
 1 5 10 15  
 Thr Pro Ala Ser Gly Gly Thr Ser Leu His Thr Pro Arg Ser Arg Pro  
 20 25 30  
 Ser Ser Pro Gly Pro Ser Thr Trp Ala Gly Ser Gln Leu Ser Ser Cys  
 35 40 45  
 Ser Val  
 50

<210> 101  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

<400> 101  
 Ala Gly Lys Asp Ser Gly Leu Asp  
 1 5

<210> 102  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
 Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe Gly  
 1 5 10 15  
 Ile Trp Ile Leu Ile  
 20

<210> 103  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 103  
 Val Leu Ala Ile Ser Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly  
 1 5 10 15  
 Cys Val Gly Ala Leu  
 20

<210> 104  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Leu Tyr Phe Gly Met Leu Leu Leu Leu Phe Ala Thr Gln Ile Thr Leu  
 1 5 10 15  
 Gly Ile Leu Ile Ser  
 20



<210> 105  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 105  
 Ala Ser Asp Val Leu Glu Leu Thr Asp Asp Asn Phe Glu Ser Arg Ile  
 1 5 10 15  
 Ser Asp Thr Gly Ser Ala Gly Leu Met Leu Val Glu Phe Phe Ala Pro  
 20 25 30  
 Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Tyr Glu Ala Ala Ala  
 35 40 45  
 Thr Arg Leu Lys Gly Ile Val Pro Leu Ala Lys Val Asp Cys Thr Ala  
 50 55 60  
 Asn Thr Asn Thr Cys Asn Lys Tyr Gly Val Ser Gly Tyr Pro Thr Leu  
 65 70 75 80  
 Lys Ile Phe Arg Asp Gly Glu Glu Ala Gly Ala Tyr Asp Gly Pro Arg  
 85 90 95  
 Thr Ala Asp Gly Ile Val Ser His Leu Lys Lys Gln Ala Gly  
 100 105 110

<210> 106  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 106  
 Asp Gly Pro Val Lys Val Val Val Ala Glu Asn Phe Asp Glu Ile Val  
 1 5 10 15  
 Asn Asn Glu Asn Lys Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys  
 20 25 30  
 Gly His Cys Lys Asn Leu Glu Pro Lys Tyr Lys Glu Leu Gly Glu Lys  
 35 40 45  
 Leu Ser Lys Asp Pro Asn Ile Val Ile Ala Lys Met Asp Ala Thr Ala  
 50 55 60  
 Asn Asp Val Pro Ser Pro Tyr Glu Val Arg Gly Phe Pro Thr Ile Tyr  
 65 70 75 80  
 Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro Lys Lys Tyr Glu Gly Gly  
 85 90 95  
 Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu Gln Arg Glu Ala Thr  
 100 105 110

<210> 107  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 107  
 Ser Asp Thr Gly Ser Ala Gly Leu Met Leu Val Glu Phe Phe Ala Pro  
 1 5 10 15  
 Trp Cys Gly His Cys  
 20

<210> 108  
 <211> 160

<212> PRT

<213> Homo sapiens

<400> 108

```

Ile Gly Glu Ile Ala Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg
1           5           10           15
Thr Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser
           20           25           30
Leu Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu
           35           40           45
Lys Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys
           50           55           60
Met Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser
65           70           75           80
Gln Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp
           85           90           95
Pro Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val
           100          105          110
Leu Tyr Glu Ala Ser Pro Ala Gly Ser Thr Gln Asn Ser Thr Asn
           115          120          125
Val Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu
           130          135          140
Gly Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser
145          150          155          160

```

<210> 109

<211> 4

<212> PRT

<213> Homo sapiens

<400> 109

Val Thr Gly Gly

1

<210> 110

<211> 4

<212> PRT

<213> Homo sapiens

<400> 110

Thr Gly Gly Phe

1

<210> 111

<211> 4

<212> PRT

<213> Homo sapiens

<400> 111

Gly Gly Phe Ser

1

<210> 112

<211> 6

<212> PRT

<213> Homo sapiens

<400> 112

Val Thr Gly Gly Phe Ser  
1 5

<210> 113

<211> 4

<212> PRT

<213> Homo sapiens

<400> 113

Met Pro Leu Pro  
1

<210> 114

<211> 4

<212> PRT

<213> Homo sapiens

<400> 114

Pro Leu Pro Leu  
1

<210> 115

<211> 4

<212> PRT

<213> Homo sapiens

<400> 115

Pro Leu Pro Ser  
1

<210> 116

<211> 4

<212> PRT

<213> Homo sapiens

<400> 116

Leu Pro Ser Ala  
1

<210> 117

<211> 8

<212> PRT

<213> Homo sapiens

<400> 117

Met Pro Leu Pro Leu Pro Ser Ala  
1 5

<210> 118

<211> 1161

<212> DNA

<213> Homo sapiens

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<400> 118
ggaaaactat gcctggggcc gacgctctgc ccggtgctg ccgctgagga aagccgggac      60
gcggagcccc gccgagagct tctttgctcc ggacgcccct ggacgtggcg ggcagccgcg    120
agggtaacca ccatgatccc ctgggtgctc ctggcctgtg ccctcccctg tgctgctgac    180
ccactgcttg gcgcctttgc tcgcagggaac ttccggaaaag gctcccctca actggtctgc    240
agcctgcttg gccccaggga cccaccgggc ccccaggag ccccaggggc ctcaggaatg    300
atgggacgaa tgggctttcc tggcaaagac ggccaagatg gacacgacgg cgaccggggg    360
gacagcggag aggaaggtcc acctggccgg acaggtaacc ggggaaagcc aggaccaaag    420
ggcaaagccg gggccattgg gcgggctggc ccccgaggcc ccaagggggg caacgggtacc    480
cccgggaagc atggcacacc aggcaagaag gggcccaagg gcaagaaagg ggagccaggc    540
ctcccaggcc cctgcagctg tggcagtggc cataccaagt cagctttctc ggtggcagtg    600
accaagagct acccacggga gcggctgccc atcaagtttg acaagattct gatgaacgag    660
ggtggccact acaatgcttc cagcggcaag ttcgtctgcg gcgtgcctgg gatctactac    720
ttcacctacg acatcacgct ggccaacaag cacctggcca tcggcctggg gcacaacggc    780
cagtaccgca tccggacctt tgatgccaac accggcaacc acgatgtggc ctcaggctcc    840
accatcctgg ctctcaagca gggtgacgaa gtttggtctg agatcttcta ctcagagcag    900
aacgggctct tctatgacct ttactggaca gacagcctct ttacgggctt cctaattctat    960
gccgaccagg atgaccccaa cgaggtatag acatgccacg gcggtcctcc aggcagggaa   1020
caagcttctg gacttgggct tacagagcaa gacccacaa ctgtaggctg ggggtggggg   1080
gtcaggtgag cggttctagc ctcaggctca cctcctccgc ctcttttttt ccccttcatt   1140
aatccaac   cttttattc a                                     1161

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<210> 119
<211> 285
<212> PRT
<213> Homo sapiens

```

```

<400> 119
Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
1           5           10          15
Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys Gly Ser Pro
20          25          30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
35          40          45
Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly Phe Pro Gly
50          55          60
Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp Ser Gly Glu
65          70          75          80
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro Gly Pro Lys
85          90          95
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly
100         105         110
Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys Lys Gly Pro
115         120         125
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly
130         135         140
Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr Lys Ser Tyr
145         150         155         160
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu
165         170         175
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Gly Val Pro
180         185         190
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu
195         200         205

```

Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp  
 210 215 220  
 Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala  
 225 230 235 240  
 Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln  
 245 250 255  
 Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly  
 260 265 270  
 Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val  
 275 280 285

<210> 120

<211> 886

<212> DNA

<213> Homo sapiens

<400> 120

gaattcggca cgagggccgc gagggtaacc accatgatcc cctgggtgct cctggcctgt 60  
 gccctcccct gtgctgctga cccactgctt ggcgcccttg ctgcgaggga cttccggaaa 120  
 ggctcccctc aactggtctg cagcctgcct ggcccccagg gccaccgagg cccccagga 180  
 gccccagggc cctcaggaat gatgggacga atgggctttc ctggcaaaga cggccaagat 240  
 ggacacgacg gcgaccgggg ggacagcgga gaggaaggct cacctggccg gacagtgacc 300  
 aagagctacc cacgggagcg gctgcccata aagtttgaca agattctgat gaacgagggt 360  
 ggccactaca atgcttcag cggaagttc gtctgcggcg tgcctgggat ctactacttc 420  
 acctacgaca tcacgctggc caacaagcac ctggccatcg gcctggtgca caacggccag 480  
 taccgcatcc ggacctttga tgccaacacc ggcaaccacg atgtggcctc aggtccacc 540  
 atcctggctc tcaagcaggg tgacgaagtt tggctgcaga tcttctactc agagcagaac 600  
 gggctcttct atgacctta ctggacagac agcctcttta cgggcttctc aatctatgcc 660  
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<211> 217

<212> PRT

<213> Homo sapiens

<400> 121

Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp  
 1 5 10 15  
 Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys Gly Ser Pro  
 20 25 30  
 Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro  
 35 40 45  
 Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly Phe Pro Gly  
 50 55 60  
 Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp Ser Gly Glu  
 65 70 75 80  
 Glu Gly Pro Pro Gly Arg Thr Val Thr Lys Ser Tyr Pro Arg Glu Arg  
 85 90 95  
 Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr  
 100 105 110  
 Asn Ala Ser Ser Gly Lys Phe Val Cys Gly Val Pro Gly Ile Tyr Tyr  
 115 120 125

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Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu
   130               135               140
Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly
145               150               155               160
Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Gln Gly
               165               170               175
Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe
               180               185               190
Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr
               195               200               205
Ala Asp Gln Asp Asp Pro Asn Glu Val
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<210> 122
<211> 15
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<213> Homo sapiens

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<220>
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1               5               10               15

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<400> 123
Ser His His His
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<210> 124  
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<400> 124  
Ala Ala Asn Ser Lys Val Ala Phe Ser Ala Val Arg Ser Thr Asn His  
1 5 10 15

<210> 125  
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<212> PRT  
<213> Homo sapiens

<400> 125  
Ala Ala Asn Ser Lys Val Ala Phe Ser Ala Val Arg  
1 5 10

<210> 126  
<211> 4  
<212> PRT  
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<400> 126  
Ser Thr Asn His  
1

<210> 127  
<211> 16  
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<400> 127  
Ser Gly Ser Ala Lys Val Ala Phe Ser Ala Thr Arg Ser Thr Asn His  
1 5 10 15